



Respiratory Viruses in the Tropics

November 8, 2013

Leyi Lin, MD, FACP
Viral Diseases Branch
WRAIR



Outline

- Influenza
 - Introduction
 - ‘Seasonal’ influenza in the tropics
 - Pandemic Influenza
 - Avian Influenza
- Other respiratory viruses
- Respiratory viruses with high mortality
- Summary

Influenza Virus

- Family: Orthomyxoviridae
- First isolated 1933
- Segmented genome
- 8 single stranded, negative sense RNA molecules
- Encodes for 10 proteins
 - Nucleoprotein (NP), Matrix (M) protein
 - Important surface glycoproteins
 - Hemagglutinin (HA)
 - Neuraminidase (NA)

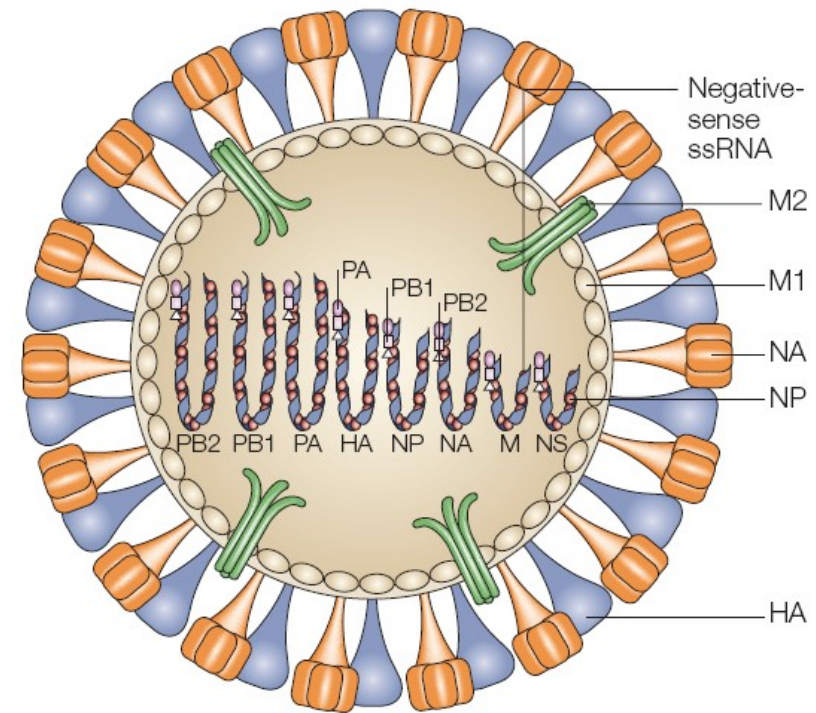


Figure 1 | **Schematic diagram of an influenza A virus virion.** Two surface glycoproteins, haemagglutinin (HA) and neuraminidase (NA), and the M2 ion-channel protein are embedded in the viral envelope, which is derived from the host plasma membrane. The ribonucleoprotein complex comprises a viral RNA segment associated with the nucleoprotein (NP) and three polymerase proteins (PA, PB1 and PB2). The matrix (M1) protein is associated with both ribonucleoprotein and the viral envelope. A small amount of non-structural protein 2 is also present, but its location within the virion is unknown.



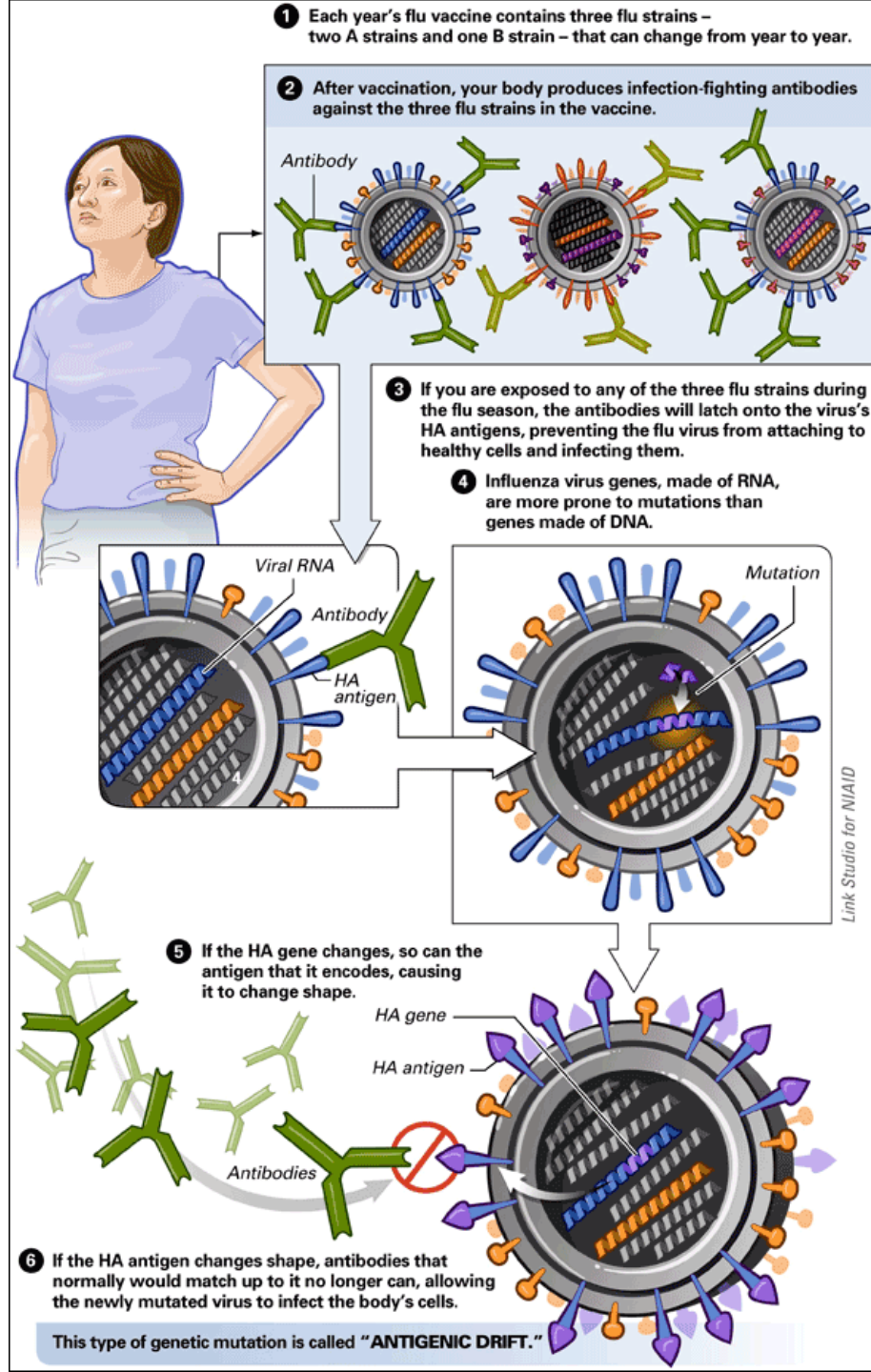
HA and NA

- Hemagglutinin initiates infection by binding to sialic acid residue on respiratory epithelial cells
- Neuraminidase liberates new virions after viral replication and help virions stay separated



Antigenic Drift

- Occurs in Influenza A and B
- Point mutations in the viral RNA genes
- Leads to production of new hemagglutinin or neuraminidase
- Annual occurrence to avoid host immune system
- Less severe 'seasonal' epidemics
- Occurs as virus spreads through a susceptible population



<http://nieman.harvard.edu/Microsites/NiemanGuideToCoveringPandemicFlu/TheScience/HowFluVirusesChange>

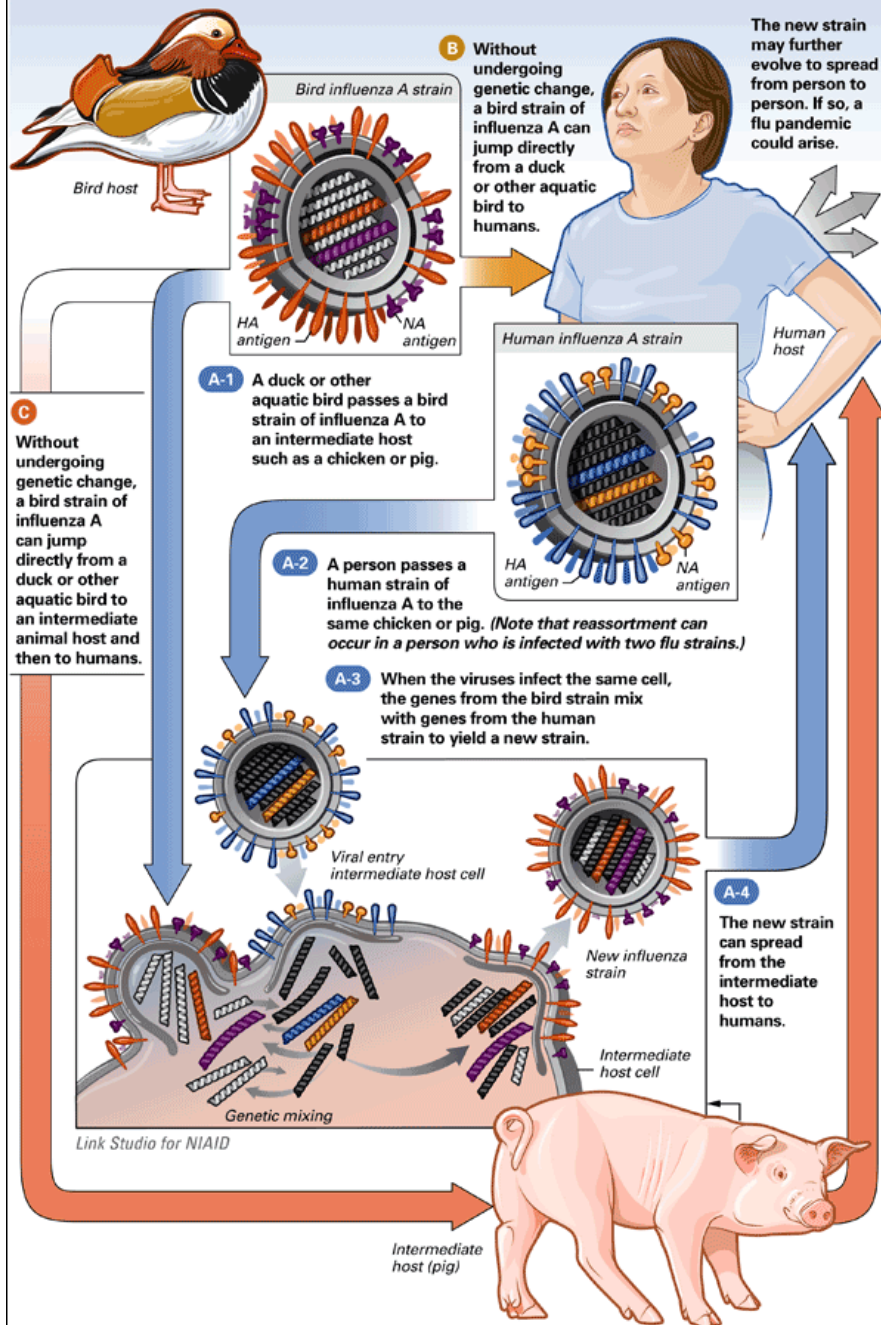


Antigenic Shift

- Major changes in HA and NA
- Influenza A viruses only
- Reassortment of viral genetic material between viruses co-infecting the same cell
- **Pandemic strains** result from exchange of genetic material between animal and human viruses
- No protective immunity in host
- Usually more rapidly spreading and severe infection







































































































The genetic change that enables a flu strain to jump from one animal species to another, including humans, is called “**ANTIGENIC SHIFT**.” Antigenic shift can happen in three ways:



<http://nieman.harvard.edu/Microsites/NiemanGuideToCoveringPandemicFlu/TheScience/HowFluVirusesChange>



- All HA and NA in birds
- Crossing of species is limited
 - Humans
 - H1, H2, H3
 - N1, N2
 - Horses
 - H7, N7
 - H3, N8
 - Pigs
 - H1, H3
 - N1, N2

Haemagglutinin subtypes			Neuraminidase subtypes		
H1	   		N1	   	
H2	   		N2	   	
H3	    		N3	   	
H4	   		N4	   	
H5	   		N5	   	
H6	   		N6	   	
H7	    		N7	    	
H8	   		N8	    	
H9	   		N9	   	
H10	   				
H11	   				
H12	   				
H13	   				
H14	   				
H15	   				





Influenza Typing

- Classified based on antigenic differences in NP and M
- Influenza A viruses have various types of HA and NA
- Influenza B viruses do NOT have shifts and major changes in HA and NA
- Example Nomenclature

Type / **Host** / **Place** / **Strain #** / **Year** (Influenza subtype)

A / **Duck** / **Vietnam** / **11** / **04** (H5N1)



Influenza in the Tropics

- Less distinct 'seasonal' pattern vs. temperate regions
- Year round infections
- 'seasonal' patterns vary by location
 - Peaks related to rainy seasons
 - Biannual peaks (rainy season and winter months)
 - Year round infection without clear peaks



Environmental Predictors of Seasonal Influenza Epidemics across Temperate and Tropical Climates

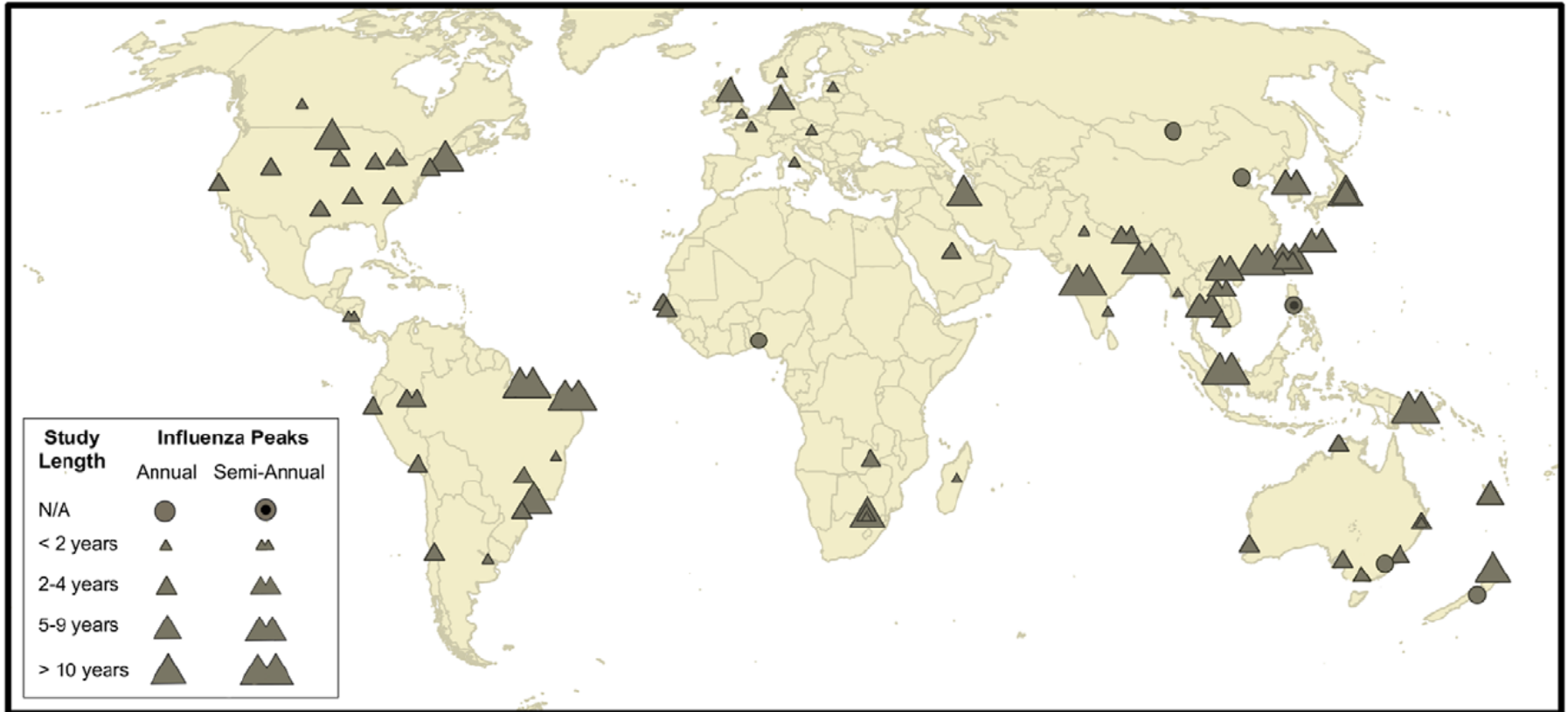
- Study conducted at 78 study sites globally
- Influenza infections peaked during low specific humidity and temperatures in areas where these values fell below threshold
- In areas with constant high humidity and temperature, influenza infections peaked in month of high precipitation

Citation: Tamerius JD, Shaman J, Alonso WJ, Bloom-Feshbach K, Uejio CK, et al. (2013) Environmental Predictors of Seasonal Influenza Epidemics across Temperate and Tropical Climates. PLoS Pathog 9(3): e1003194. doi:10.1371/journal.ppat.1003194

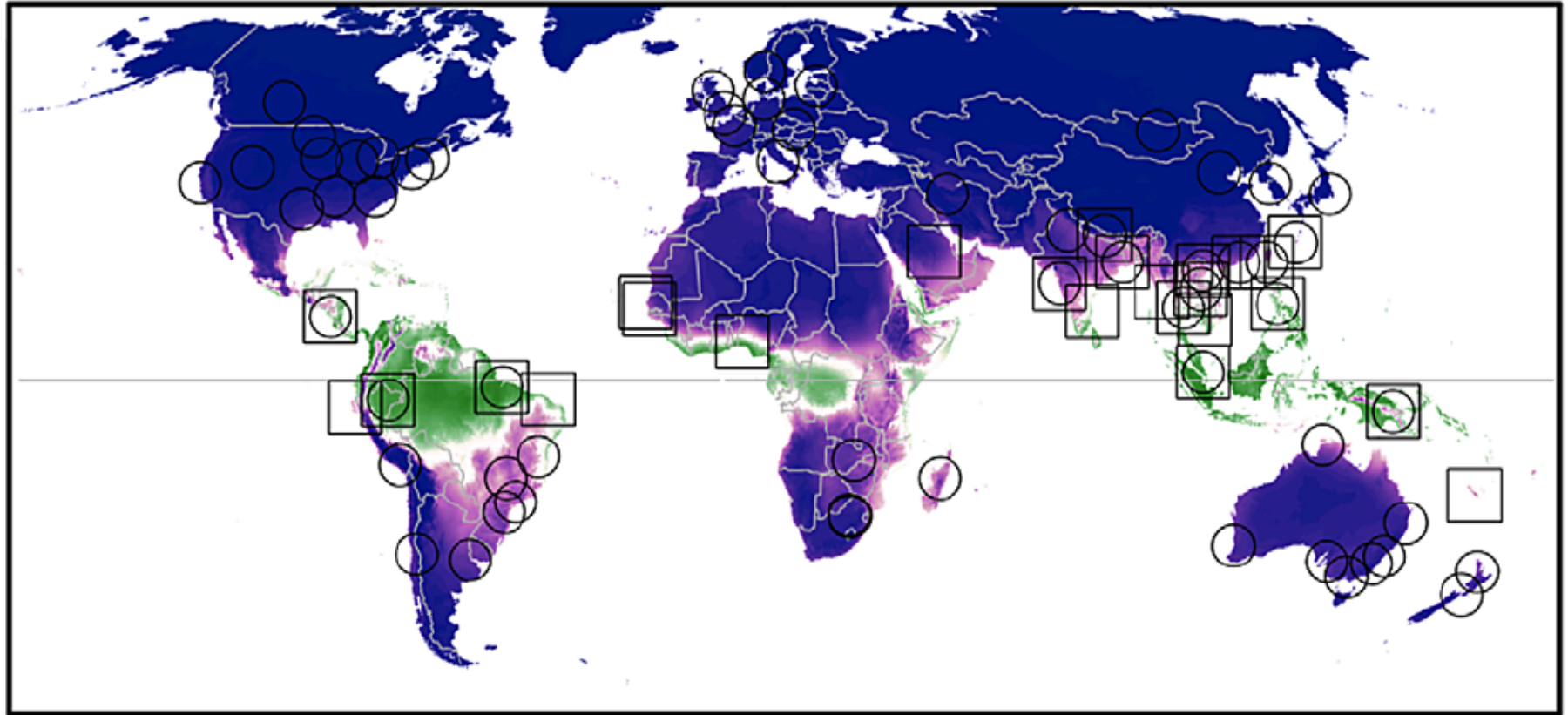
Editor: Steven Riley, Imperial College London, United Kingdom

Received August 28, 2012; **Accepted** December 26, 2012; **Published** March 7, 2013

Influenza in the tropics



Influenza in the tropics



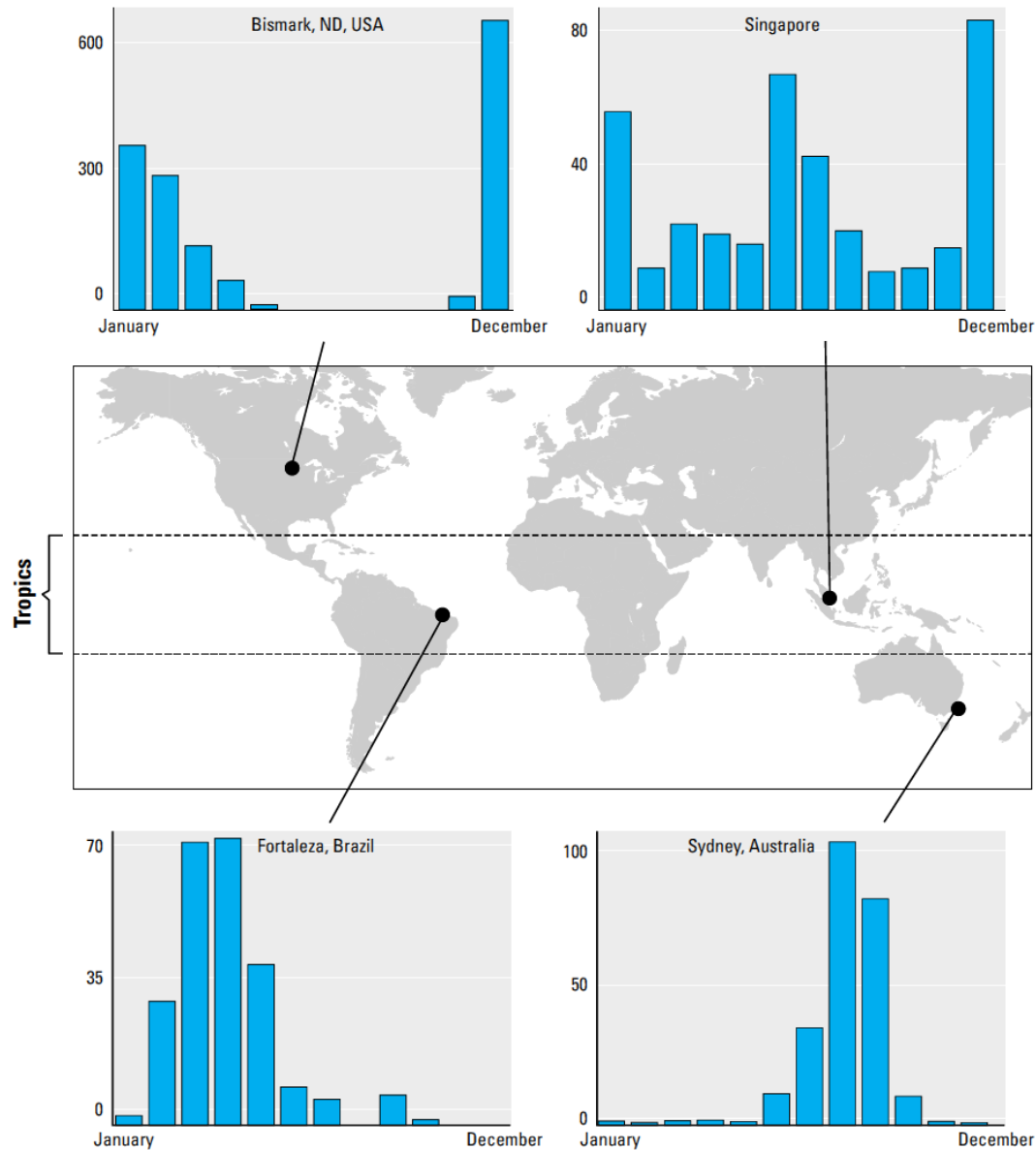
Cold-Dry Peaks



Humid-Rainy Peaks



Rainy season = influenza peak



Tamerius et al.
*Environ Health
Perspect* 2011



Multiple Factors Impact Influenza Epidemics

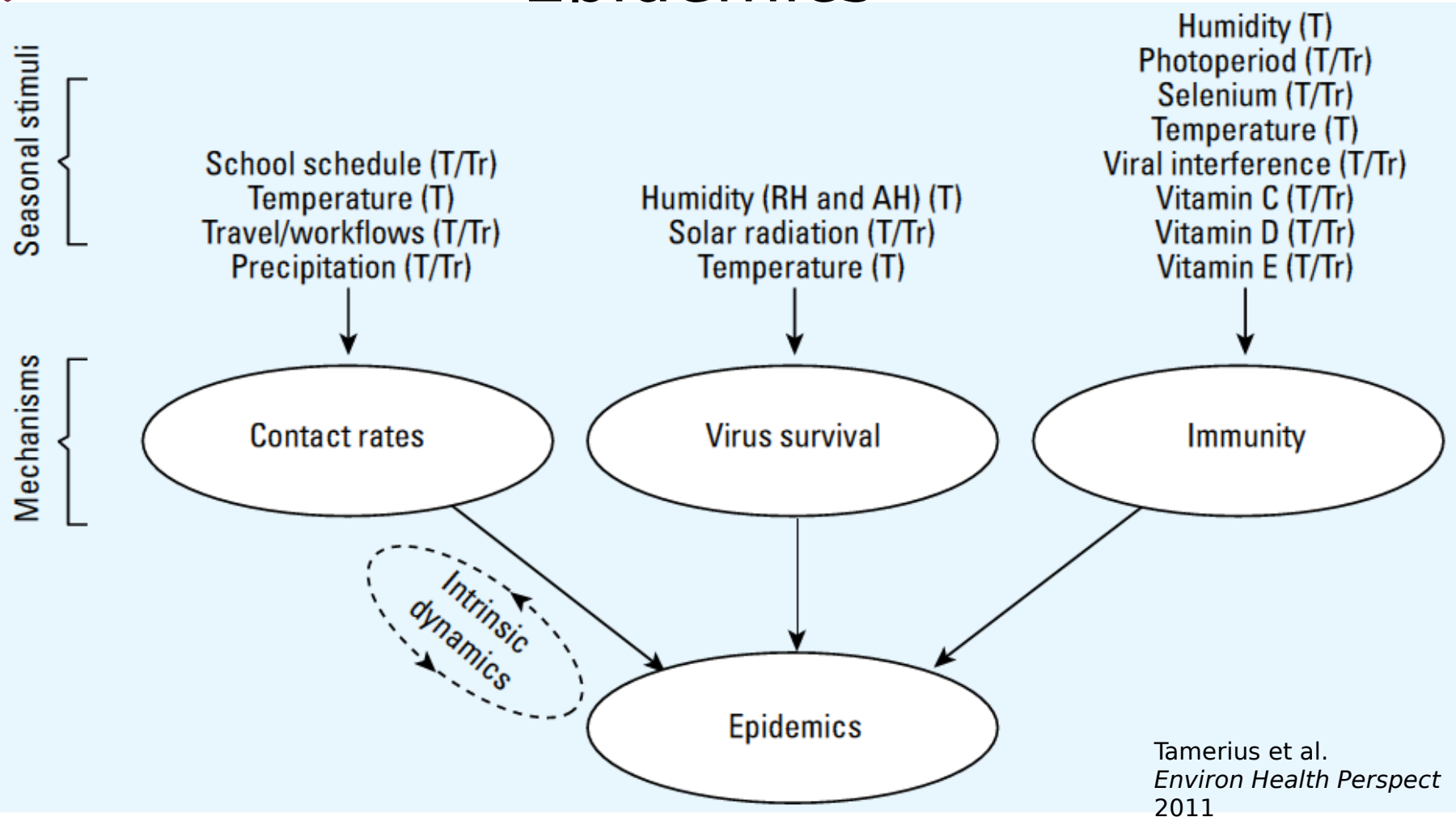


Figure 2. Putative relationship and causal connections among key seasonal stimuli, mediating mechanisms, and influenza epidemics. The notation adjacent to each seasonal stimulus indicates whether it potentially explains influenza seasonality in the tropics (Tr), temperate regions (T), or both (T/Tr). The diagram also includes a component depicting the effects of intrinsic dynamics.



Seasonal Influenza Vaccine



- Surveillance at 130 influenza centers in 101 countries
- WHO centers (Atlanta, London, Melbourne, Tokyo, Beijing)
- Meetings and decision for inclusion:
 - September for Southern hemisphere's vaccine
 - February for Northern hemisphere's vaccine
- WHO recommended 2013-2014 vaccine:
 - An A/California/7/2009 (H1N1) pdm09-like virus
 - An A(H3N2) virus similar to A/Victoria/361/2001
 - CDC: A/Texas/50/2012
 - A B/Massachusetts/2/2012-like virus
 - A B/Brisbane/60/2008-like virus **
- Identify strain to be used, growing virus strain, quality control, production, sale, distribution, administration
- TAKES TIME (at least 6 months) and MISMATCHES OCCUR

Vaccine Efficacy

	Population (dates)	Patients randomly allocated to receive TIV and placebo	Vaccine efficacy (95% CI)	Reported antigenic match
Adults (18–64 years)				
Ohmit et al (2006) ²⁴	Healthy adults aged 18–46 years (2004–05)	728	75% (42 to 90)	Type A: drifted H3N2; type B: mixed lineage
Ohmit et al (2008) ²⁵	Healthy adults aged 18–48 years (2005–06)	1205	16% (–171 to 70)	Type A: drifted H3N2; type B: lineage mismatch (1 isolate)
Beran et al (2009) ²⁶	Healthy adults aged 18–64 years (2005–06)	6203	22% (–49 to 59)	Type A: similar H3N2 and H1N1; type B: lineage mismatch
Beran et al (2009) ²⁷	Healthy adults aged 18–64 years (2006–07)	7652	62% (46 to 73)	Type A: similar H3N2; type B: lineage mismatch
Monto et al (2009) ²⁸	Healthy adults aged 18–49 years (2007–08)	1139	68% (46 to 81)	Type A: drifted H3N2; type B: lineage mismatch
Jackson et al (2010) ²¹	Healthy adults aged 18–49 years (2005–06)	3514	50%† (14 to 71)	Type A: similar H3N2; type B: lineage mismatch
Jackson et al (2010) ²¹	Healthy adults aged 18–49 years (2006–07)	4144	50%† (–3 to 75)	Type A: similar H3N2; type B: mixed lineage
Frey et al (2010) ²⁹	Healthy adults aged 18–49 years (2007–08)	7576	63% (one-sided 97.5% lower limit of 47%)	Type A: mixed strains; type B: lineage mismatch
Madhi et al (2011) ³⁰	Adults aged 18–55 years with HIV infection (2008–09)	506	76% (9 to 96)	Type A: drifted H1N1; type B: not reported
Children (6–24 months)				
Hoberman et al (2003) ³¹	Healthy children aged 6–24 months (1999–2000)	411	66% (34 to 82)	Type A: similar H3N2 and H1N1; type B: not reported
Hoberman et al (2003) ³¹	Healthy children aged 6–24 months (2000–01)	375	–7% (–247 to 67)	Type A: similar H3N2 and H1N1; type B: lineage match

No studies were available for adults aged 65 years or older or children aged 2–17 years. *One other study by Loeb and colleagues⁴⁸ met inclusion criteria and contained data for all age groups. †Our calculation.

Table 2: Randomised controlled trials of trivalent inactivated vaccine (TIV) meeting inclusion criteria*



Vaccine Efficacy

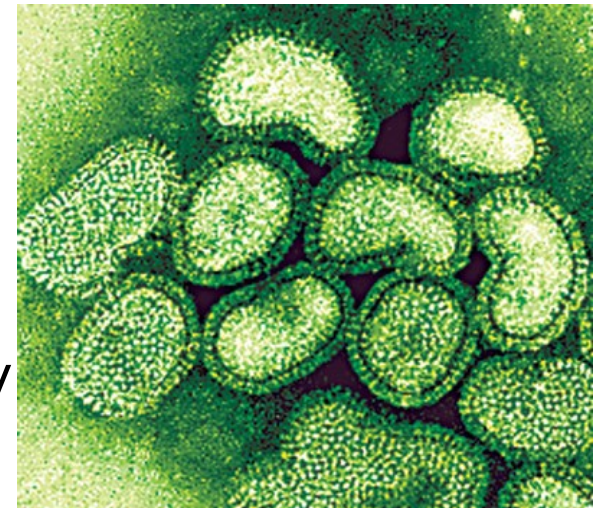
	Population (dates)	Patients randomly allocated to receive LAIV and placebo	Vaccine efficacy (95% CI)	Reported antigenic match
Adults (≥60 years)				
De Villiers et al (2010) ³⁷	Community-dwelling ambulatory adults aged ≥60 years (2001–02)	3242	Overall 42% (21 to 57); 31% (–3 to 53) for patients aged 60–69 years; 57% (29 to 75) for patients aged ≥70 years	Type A: similar H3N2; type B: lineage match
Adults (18–49 years)				
Ohmit et al (2006) ²⁴	Healthy adults aged 18–46 years (2004–05)	725	48% (–7 to 74)	Type A: drifted H3N2; type B: mixed lineage
Ohmit et al (2008) ²⁵	Healthy adults aged 18–48 years (2005–06)	1191	8% (–194 to 67)	Type A: drifted H3N2; type B: lineage mismatch (1 isolate)
Monto et al (2009) ^{28*}	Healthy adults aged 18–49 years (2007–08)	1138	36% (0 to 59)	Type A: drifted H3N2; type B: lineage mismatch
Children (6 months–7 years)				
Belshe et al (1998) ³²	Healthy children aged 15–71 months (1996–97)	1602	93% (88 to 96)	Type A: similar H3N2; type B: lineage match
Belshe et al (2000) ³³	Healthy children aged 26–85 months (1997–98)	1358	87% (78 to 93)	Type A: drifted H3N2; type B: not reported (1 isolate)
Vesikari et al (2006) ³⁴	Healthy children aged 6–<36 months attending day care (2000–01)	1784	84% (74 to 90)	Type A: similar H3N2 and H1N1; type B: lineage match
Vesikari et al (2006) ³⁴	Healthy children aged 6–<36 months attending day care (2001–02)	1119	85% (78 to 90)	Type A: similar H3N2 and H1N1; type B: mixed lineage
Bracco Neto et al (2009) ³⁸	Healthy children aged 6–<36 months (2000–01)	1886	72% (62 to 80)	Majority of strains were similar (not reported by type)
Tam et al (2007) ³⁵	Healthy children aged 12–<36 months (2000–01)	3174	68% (59 to 75)	Type A: similar H3N2 and H1N1; type B: lineage match
Tam et al (2007) ³⁵	Healthy children aged 12–<36 months (2001–02)	2947	57% (30 to 74)	Type A: similar H3N2 and H1N1; type B: mixed lineage
Lum et al (2010) ³⁶	Healthy children aged 11–<24 months (2002–03)	1233	64% (40 to 79)	Type A: similar H1N1 and mixed H3N2; type B: mixed lineage

No studies were available for adults aged 50–59 years or children aged 8–17 years. *Authors reported culture, RT-PCR, and RT-PCR/culture; we report RT-PCR/culture results.

Table 3: Randomised controlled trials of live attenuated influenza vaccine (LAIV) meeting inclusion criteria

Pandemic Influenza

- Influenza A virus introduction
 - Novel HA gene
 - No 'herd' immunity
 - Ability to spread efficiently among humans
- Pandemics of 20th century
 - All originated from avian influenza viruses
 - Intervals of 11-39 years
 - 1918 (H1N1: Spanish)
 - 1957 (H2N2: Asian)
 - 1968 (H3N2: Hong Kong)
 - 2009 (H1N1: US, Mexico)
- Pseudo- and Abortive pandemics
 - 1947 (H1N1: Japan/Korea/New Jersey)
 - 1976 (H1N1: New Jersey)
 - 1977 (H1N1: Soviet Union)





WHO Pandemic Influenza Phases

- Phases 1-3: Mostly animal infections
- Phase 4: Human-human transmission
- Phase 5-6: Pandemic, widespread human infection
- Post Peak: possibility of recurrence
- Post Pandemic: Seasonal



Pandemic Influenza

- Severe influenza syndrome
 - Fever, cough, fatigue, shortness of breath
 - Abdominal pain, diarrhea, vomiting
 - No conjunctivitis
- CXR
 - Bilateral infiltration, lobar collapse, focal consolidation
- Complications
 - Acute respiratory distress, renal failure, bacterial superinfection



1918 Influenza Pandemic

- 1/3 of the world's population (500m) infected / ill
- Case fatality rates of $>2.5\%$
- 50-100m deaths
- 3 waves: spring/summer, summer/fall, winter
- Unclear source of pandemic virus, limited capabilities

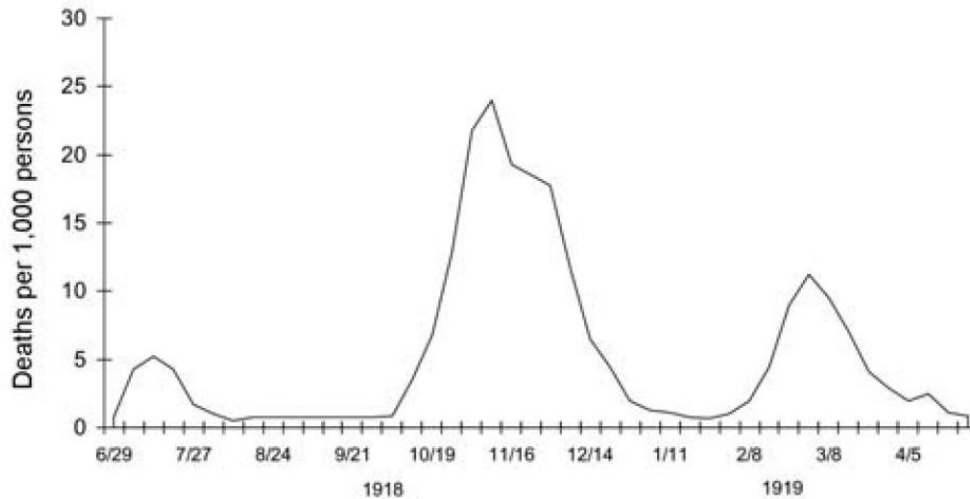


Figure 1. Three pandemic waves: weekly combined influenza and pneumonia mortality, United Kingdom, 1918–1919 (21).

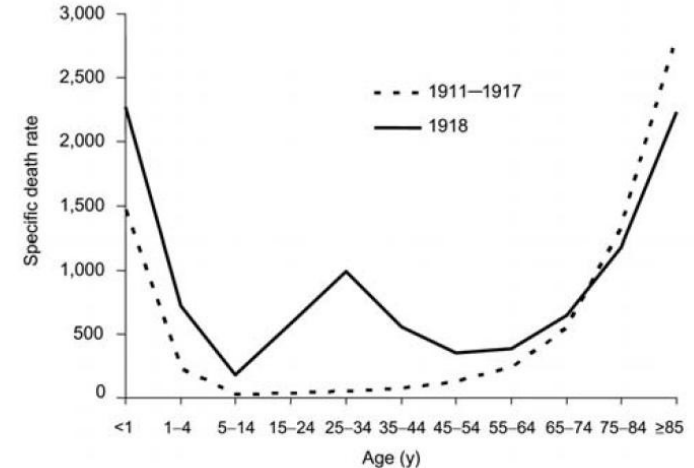


Figure 2. “U-” and “W-” shaped combined influenza and pneumonia mortality, by age at death, per 100,000 persons in each age group, United States, 1911–1918. Influenza- and pneumonia-specific death rates are plotted for the interpandemic years 1911–1917 (dashed line) and for the pandemic year 1918 (solid line) (33,34).



2009 H1N1 Pandemic



- 'Swine flu' first reported March 2009 in Mexico
- High human to human transmission, WHO pandemic level declared 6 June 2009
- Influenza A virus
 - Reassortment of 2 swine, one human strain, one avian strains
- Incubation: 1-4 days; viral shedding peak: 2-3 day into illness
- Secondary attack rate: 14-19%
- Viral shedding peaks first 2-3 days of illness
- Estimated death and impact varies by method
 - Actual deaths vs. laboratory confirmed
 - Average global H1N1 related fatality estimate: 201,200
 - CDC US H1N1 related fatality estimate: 12,470
- Less severe than 1918 H1N1 pandemic
- Immunity: natural infection, immunization, preexisting immunity from remote infection with related strain



2009 H1N1 Pandemic

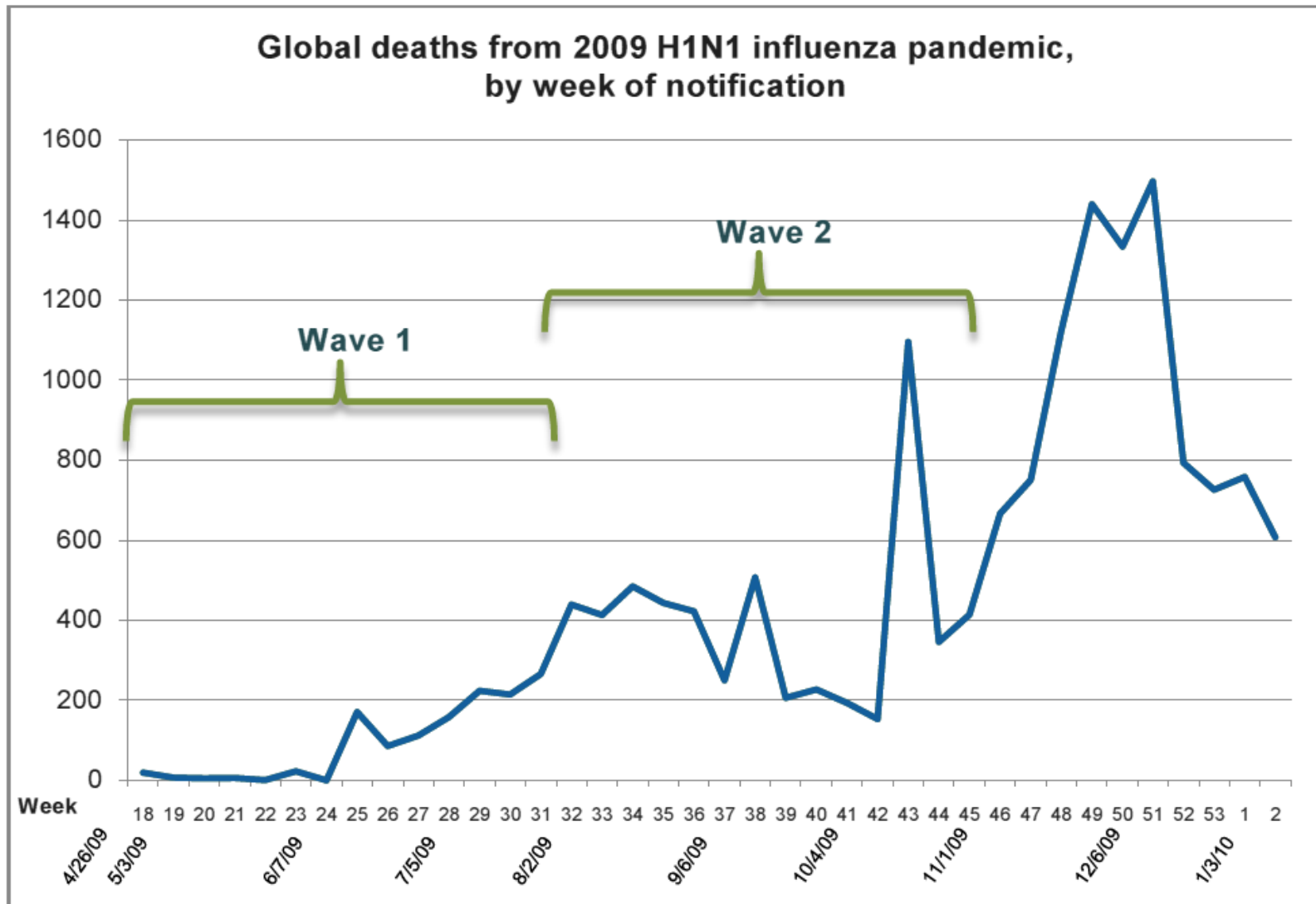


Figure 1: Global deaths from the 2009 H1N1 influenza pandemic, by week (Data Source: ECDC, 2010)

2009 H1N1 Pandemic

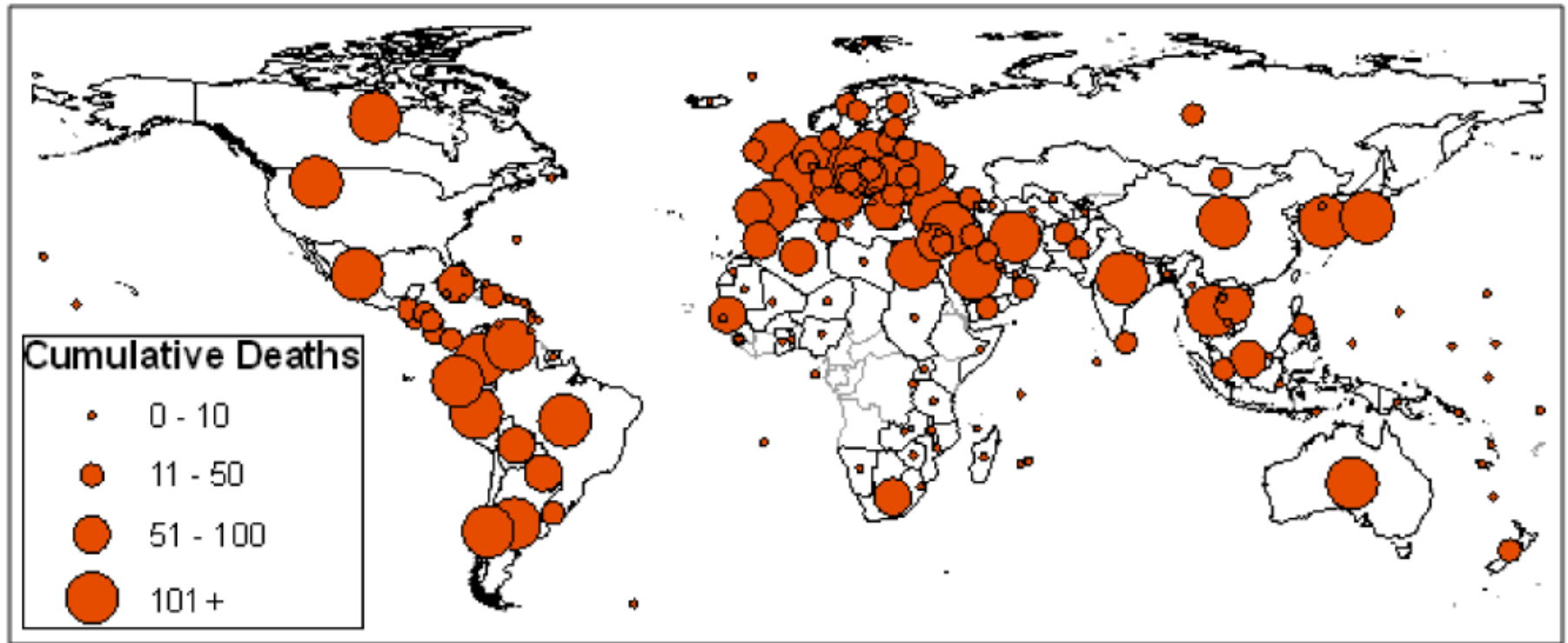


Figure 2: Map of cumulative global deaths from the 2009 H1N1 influenza pandemic, as of February 2010 (Data source: ECDC, 2010)



2009 H1N1 Pandemic

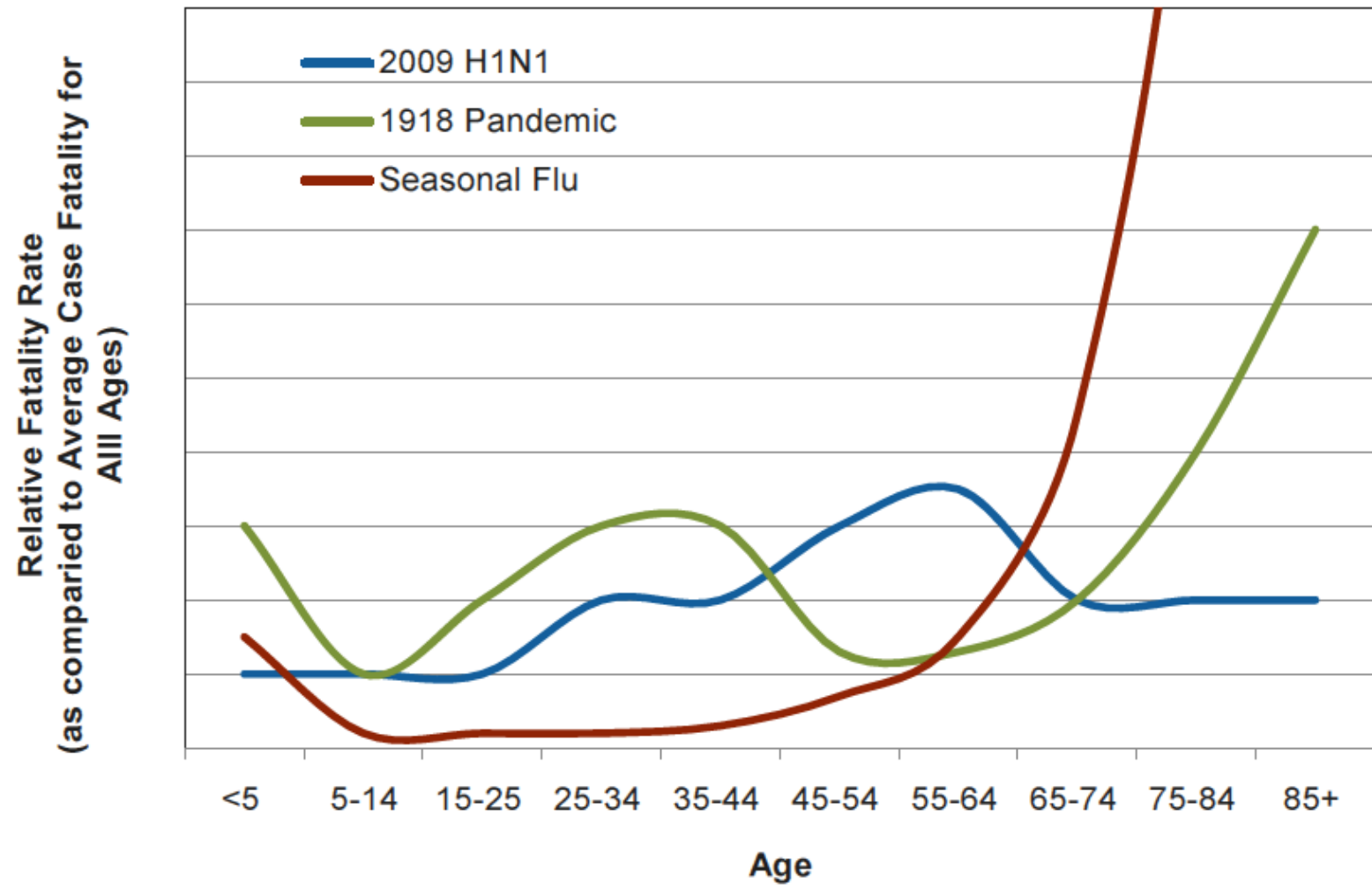
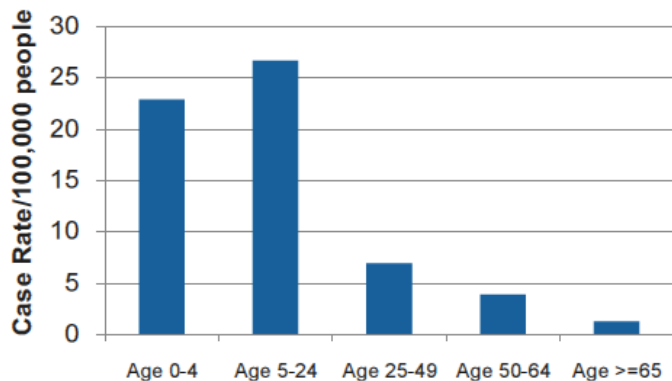


Figure 3: Age distribution of influenza mortality: comparing seasonal flu to the 1918 and 2009 pandemics

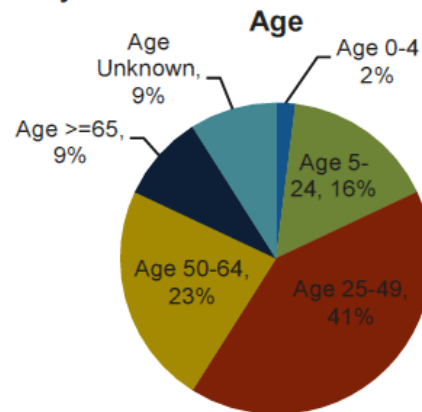


Early U.S. Cases of Novel H1N1, by Age

Estimated rates of cases per 100,000 people (from April -July 2009)



Early U.S. Deaths from Novel H1N1, by Age



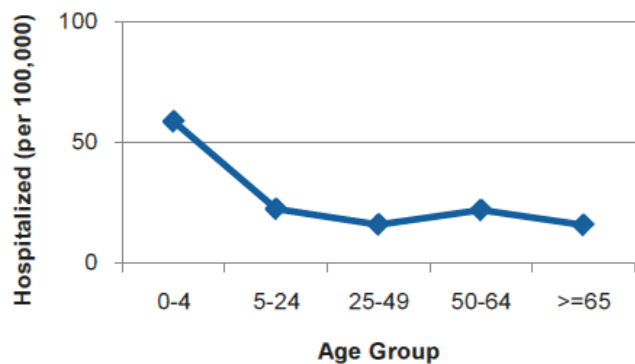
(N=268 hospitalized patients with novel H1N1 early on during outbreak)

Figure 4: Early outbreak characteristics of the 2009 H1N1 virus in the U.S.: number of cases per 100,000 people from April to July 2009 (left) and early fatalities by age (right) (Date Source: CDC, 2009).

2009 H1N1 Cumulative Lab-Confirmed Hospitalization Rate by Age Group

(n=49,008)

(April 2009 through January 30, 2010)



2009 H1N1 Cumulative Lab-Confirmed Death Rate by Age Group

(n=2,498)

(April 2009 through January 30, 2010)

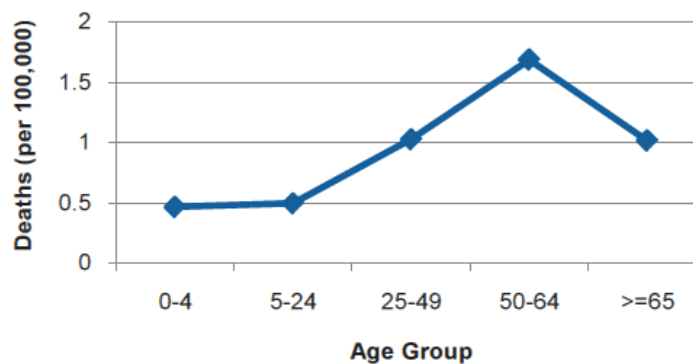


Figure 5: Age distribution of U.S. hospitalized cases (left) and fatalities (right) from the 2009 H1N1 pandemic from April 2009 through January 30, 2010 (Data Source: CDC, 2010c)



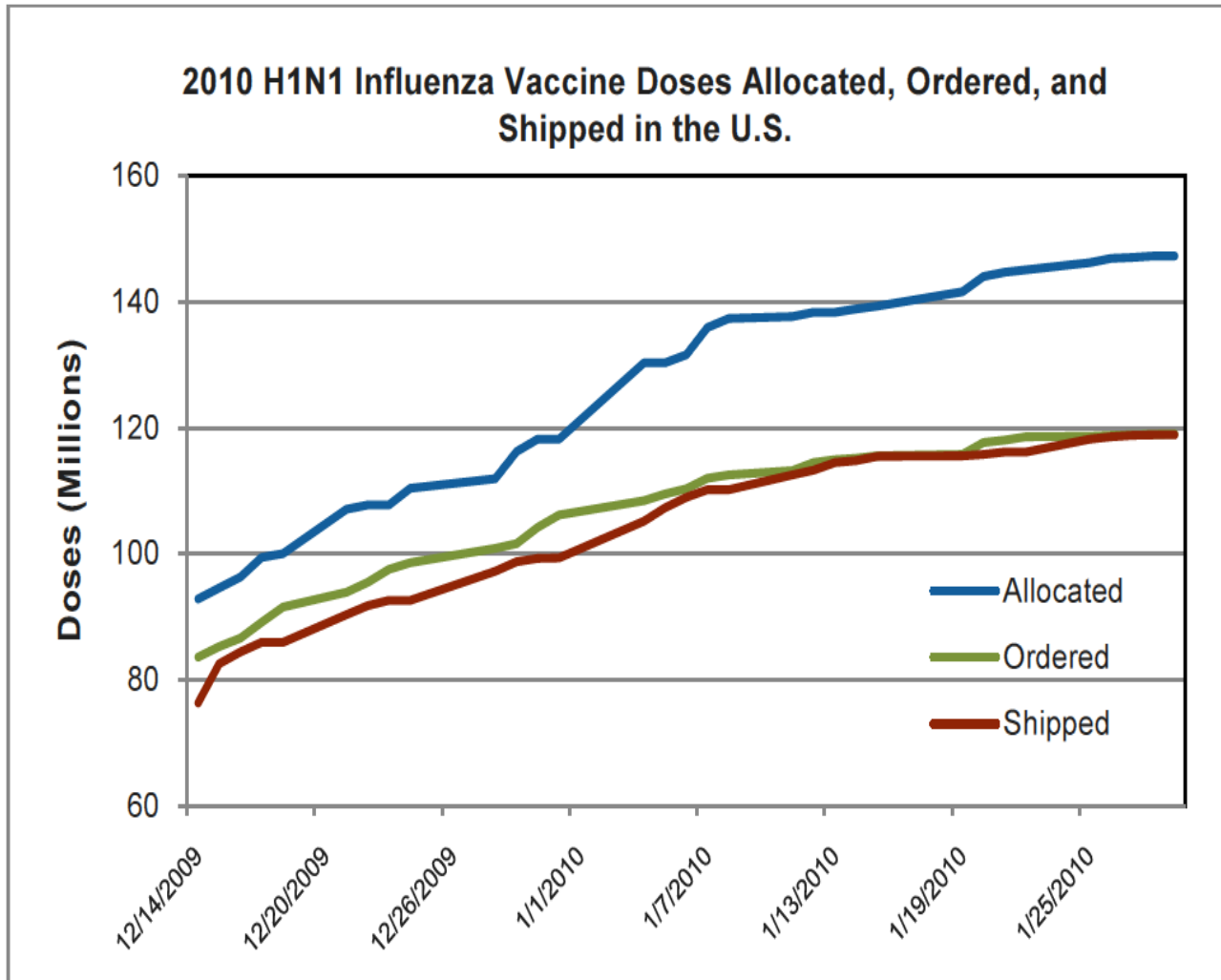
2009 H1N1 Pandemic

Table 2: Estimates of fatalities, hospitalizations, and cases for the 2009 H1N1 influenza pandemic, as modeled by RMS and estimated by the CDC as of February 13, 2010 (Data source: CDC, 2010a). Note: The CDC estimates are preliminary and do not represent the entire H1N1 pandemic. These numbers are expected to increase as more data becomes available.

Age	RMS Modeled Expected Value	CDC Lower Bound	CDC Upper Bound
Fatalities			
0-17 yrs	6,000	890	1,840
18-64 yrs	13,500	6,530	13,500
over 65 yrs	8,500	1,100	2,280
Total	28,000	8,520	17,620
Hospitalizations			
0-17 yrs	71,660	60,000	125,000
18-64 yrs	155,646	109,000	226,000
over 65 yrs	102,280	19,000	38,000
Total	329,586	188,000	389,000
Cases			
0-17 yrs	25,000,000	14,000,000	28,000,000
18-64 yrs	37,000,000	24,000,000	50,000,000
over 65 yrs	3,000,000	4,000,000	8,000,000
Total	65,000,000	42,000,000	86,000,000



Pandemic H1N1 vaccine



**March 2009:
Confirmed
H1N1 in
Veracruz,
Mexico**

**October
2009: First
H1N1
vaccine
available for
administrati
on in the
U.S.**

Figure 6: H1N1 vaccine availability in the U.S. from mid-December 2009 to end of January 2010 (Data Source: CDC, 2010)



Lessons from 2009 pandemic

- Vigilance and surveillance for novel strains
- Identify at risk population
- Limitations of laboratories and hospitals
- Educating the public about preventive measures
- Vaccine manufacturing and quality control
- Availability of antiviral drugs
- Each epidemic, pandemic is different



Avian Influenza

- Reservoir: Aquatic birds
- Transmission between birds
 - Direct
 - Indirect (fecal aerosols, water, feed, etc.)
- Clinically
 - Asymptomatic → Mild respiratory illness → Fatal systemic disease
- Most isolates are avirulent
- Epidemic fowl mortality caused by highly pathogenic variants
 - H5 and H7
 - < egg production, respiratory dz, head edema, diarrhea, death

Asian Bird Migratory Patterns

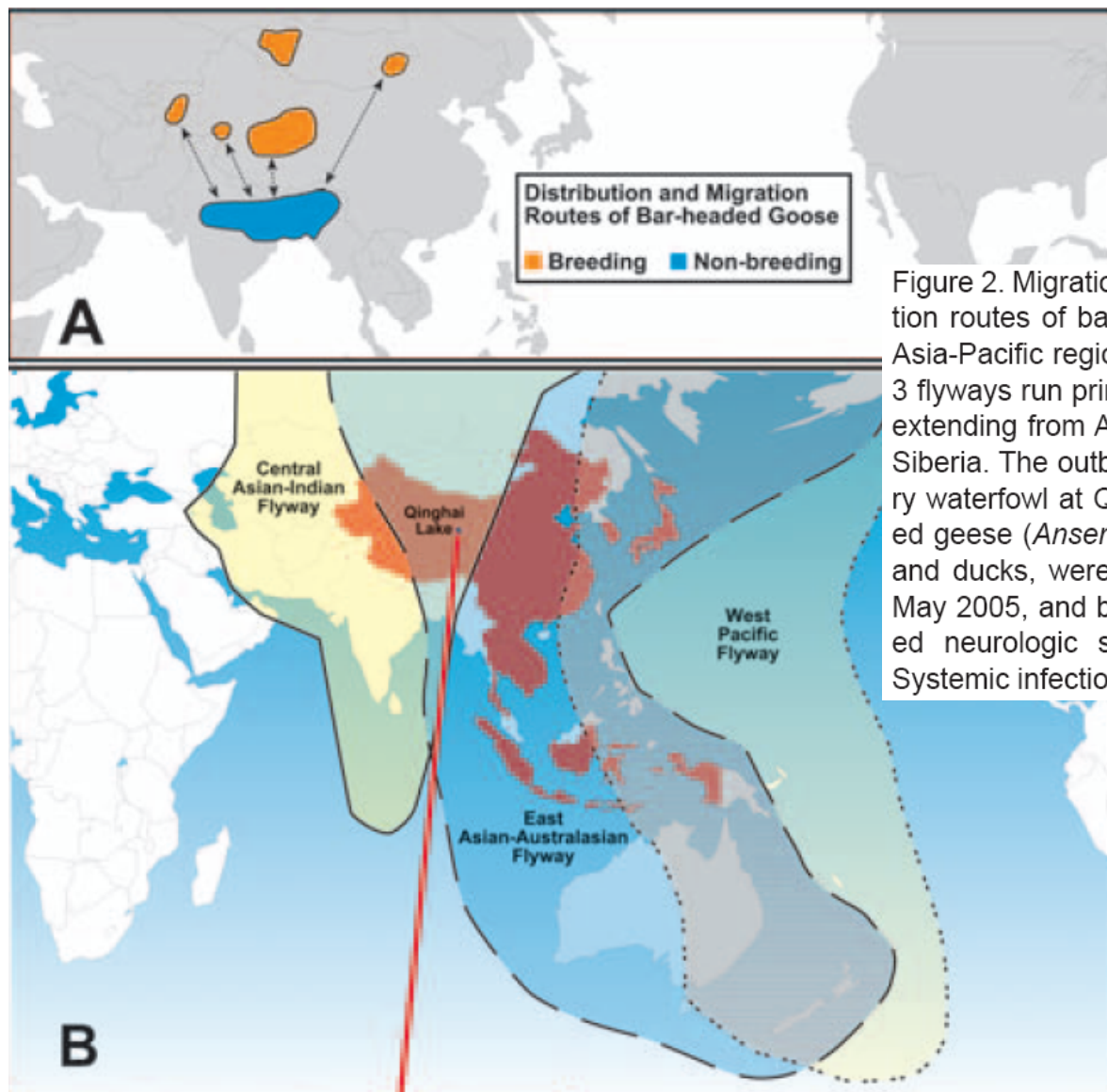


Figure 2. Migration routes of Asian birds. A) Distribution and migration routes of bar-headed geese (courtesy of P. Leader). B) The Asia-Pacific region contains >240 species of migratory birds. The 3 flyways run primarily in a north-south direction, overlapping and extending from Australia/New Zealand to India, Central Asia, and Siberia. The outbreak of highly pathogenic (HP) H5N1 in migratory waterfowl at Qinghai Lake, China, affected primarily bar-headed geese (*Anser indicus*); however, other species, including gulls and ducks, were affected (16,17). The outbreak started in early May 2005, and by June >5,000 birds had died. The birds exhibited neurologic signs, inability to stand, diarrhea, and death. Systemic infection was detected in all organs tested. C) Bar-head-



H5N1 Transmission

Table 2. Serologic and Clinical Characteristics of Avian Influenza A (H5N1) Infection among Contacts of Patients or Infected Animals.*

Group	Location	Year	Assay Method†	No. Tested	No. (%) Positive	Comment	Reference
Household contacts	Hong Kong	1997	MN, ELISA, WB	51	6 (12)	Concurrent exposure to poultry in 5 of 6 positive household contacts; 0 of 9 non-household contacts positive	Katz et al. ⁸
Tour group contacts				26	1 (4)		
Workplace contacts				47	0		
Poultry cullers	Hong Kong	1997	MN, WB	293	9 (3)	Seroconversion in 1 with mild acute respiratory illness	Bridges et al. ⁷
Poultry-market workers	Hong Kong	1997	MN, WB	1525	— (estimated 10%)	Most asymptomatic	Bridges et al. ⁷
Health care workers with contact	Hong Kong	1997	MN, WB	217	8 (4)‡	Seroconversion in 2; most asymptomatic	Buxton Bridges et al. ⁹
Household contacts§	Vietnam	2004	MN	51	0	0 of 83 controls positive	Liem et al. ¹⁰
Contacts of sick poultry§	Vietnam	2004	MN	25	0	—	
Health care workers with contact	Vietnam	2004	MN	83	0	2 with suspected illness (not confirmed)	
Health care workers with contact	Vietnam	2004	MN, RT-PCR	60	0	No recognized illness	Schultsz et al. ¹¹
Health care workers with contact§	Thailand	2004	Clinical only	54	0	No recognized illness	Apisarnthanarak et al. ¹²
Health care workers with contact	Thailand	2004	Clinical only	35	0	No fever or influenza-like illness	
Poultry cullers§	Indonesia	2005	MN	79	1 (1)	Asymptomatic	

* Some serologic surveys of apparent human-to-human transmission may have been confounded by concurrent exposure to ill poultry.

† MN denotes identification of serum antibody against influenza A (H5N1) by microneutralization, ELISA enzyme-linked immunosorbent assay, WB detection of influenza A (H5)—specific bands by Western blotting, and RT-PCR reverse-transcriptase–polymerase-chain-reaction assay for viral RNA.

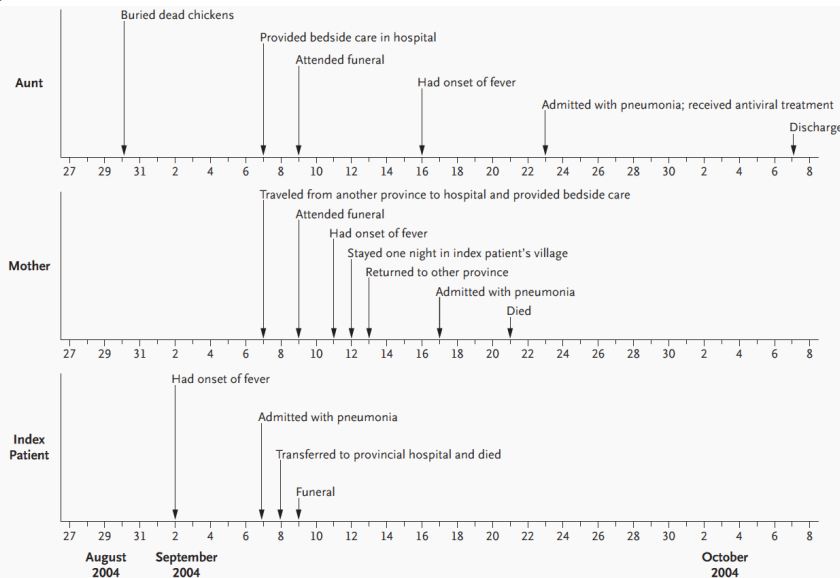
‡ P=0.01 for the comparison with 2 of 309 health care workers without contact (0.6 percent).

§ Data are from the WHO Meeting on Case Management and Research on Human Influenza A (H5) held in Hanoi, May 10 through 12, 2005.



Probable Person-to-Person Transmission of Avian Influenza A (H5N1)

N ENGL J MED 352;4 WWW.NEJM.ORG JANUARY 27, 2005



Probable person to person transmission of novel avian influenza A (H7N9) virus in Eastern China, 2013: epidemiological investigation

BMJ 2013;347:f4752 doi: 10.1136/bmj.f4752 (Published 6 August 2013)

Avian Influenza Human to Human Transmission

- A few reports of probable transmission among close family or hospital contacts

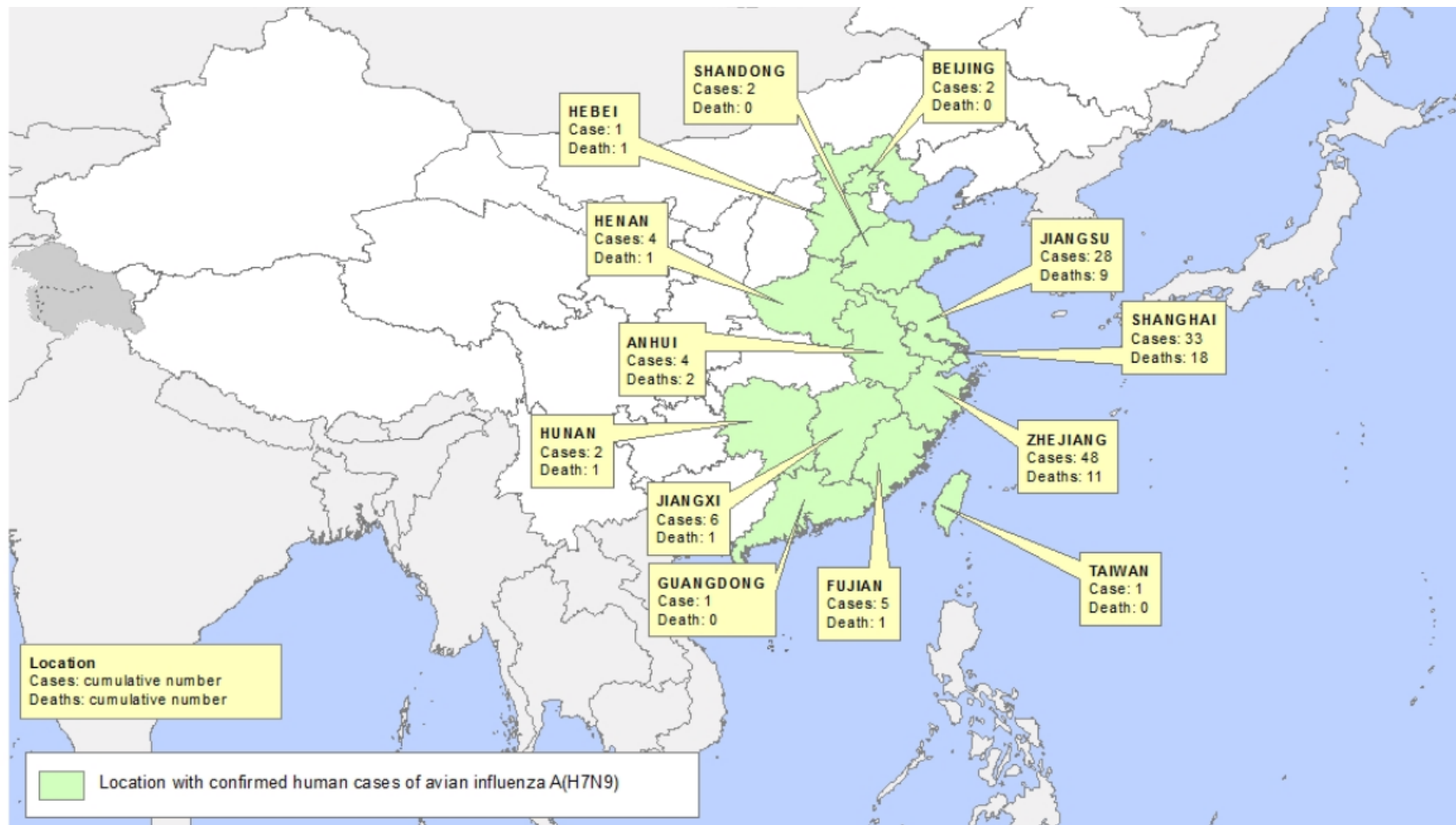


- WHO: limited non-sustained human to human spread



Avian Influenza A (H7N9)

	February		March		April		May		June		July		August		September		October		Total	
	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths
Total	4	3	33	18	94	23	2	0	0	0	2	1	0	0	0	0	2	0	137	45



Data as of 25 October 2013, 8:00 GMT+1
Source: WHO/GIP

The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not be full agreement.
©WHO 2013. All rights reserved.





Cumulative number of confirmed human cases for avian influenza A(H5N1) reported to WHO, 2003-2013

Country	2003-2009*		2010		2011		2012		2013		Total	
	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths
Azerbaijan	8	5	0	0	0	0	0	0	0	0	8	5
Bangladesh	1	0	0	0	2	0	3	0	1	1	7	1
Cambodia	9	7	1	1	8	8	3	3	20	11	41	30
China	38	25	2	1	1	1	2	1	2	2	45	30
Djibouti	1	0	0	0	0	0	0	0	0	0	1	0
Egypt	90	27	29	13	39	15	11	5	4	3	173	63
Indonesia	162	134	9	7	12	10	9	9	2	2	194	162
Iraq	3	2	0	0	0	0	0	0	0	0	3	2
Lao People's Democratic Republic	2	2	0	0	0	0	0	0	0	0	2	2
Myanmar	1	0	0	0	0	0	0	0	0	0	1	0
Nigeria	1	1	0	0	0	0	0	0	0	0	1	1
Pakistan	3	1	0	0	0	0	0	0	0	0	3	1
Thailand	25	17	0	0	0	0	0	0	0	0	25	17
Turkey	12	4	0	0	0	0	0	0	0	0	12	4
Viet Nam	112	57	7	2	0	0	4	2	2	1	125	62
Total	468	282	48	24	62	34	32	20	31	20	641	380

* 2003-2009 total figures. Breakdowns by year available on next table

Total number of cases includes number of deaths
WHO reports only laboratory cases
All dates refer to onset of illness

Source: WHO/GIP, data in HQ as of 08 October 2013



Avian Influenza

Table 1. Direct transmission of avian influenza viruses to humans

Virus subtype	Year	Location	No. cases (no. deaths)	Clinical features	Notes	Reference(s)
H5N1	1997	Hong Kong	18 (6)		Associated with outbreak of highly pathogenic AI in poultry in the region	(5,6)
H9N2	1999	Hong Kong	2 (0)	Mild influenzalike illness		(7)
H9N2	1999	Guangdong Province, China	5 (0)	Mild influenzalike illness		(8)
H9N2	2003	Hong Kong	1 (0)	Mild influenzalike illness		(9)
H5N1	2003	Hong Kong	2 (1)	Primary viral pneumonia, lymphopenia, respiratory distress	7-year-old girl died in Fujian Province, China, and H5N1 infection was not confirmed. Her 33-year-old father died from confirmed H5N1 influenza infection in Hong Kong, and her 8-year-old brother recovered from H5N1 infection.	(10)
H7N7	2003	Netherlands	89 (1)	Conjunctivitis (78 cases), mild influenzalike symptoms (2 cases) or both (5 cases). In fatal case, pneumonia followed by respiratory distress syndrome	Most cases were in persons involved in handling poultry (86), with 3 family members also affected.	(11)
H10N7	2004	Egypt	2 (0)	Fever and cough	Both cases were in infants, who recovered without complications	(12)
H5N1	2003–present	Asia (Vietnam, Thailand, Cambodia, Indonesia)	116 (60)*	Fever, respiratory symptoms, lymphopenia, elevated liver enzymes. Severe cases progress to respiratory failure, multiple organ dysfunction, and death.	Human cases concomitant with unprecedented outbreaks of highly pathogenic H5N1 AI in poultry	WHO* (13–15)

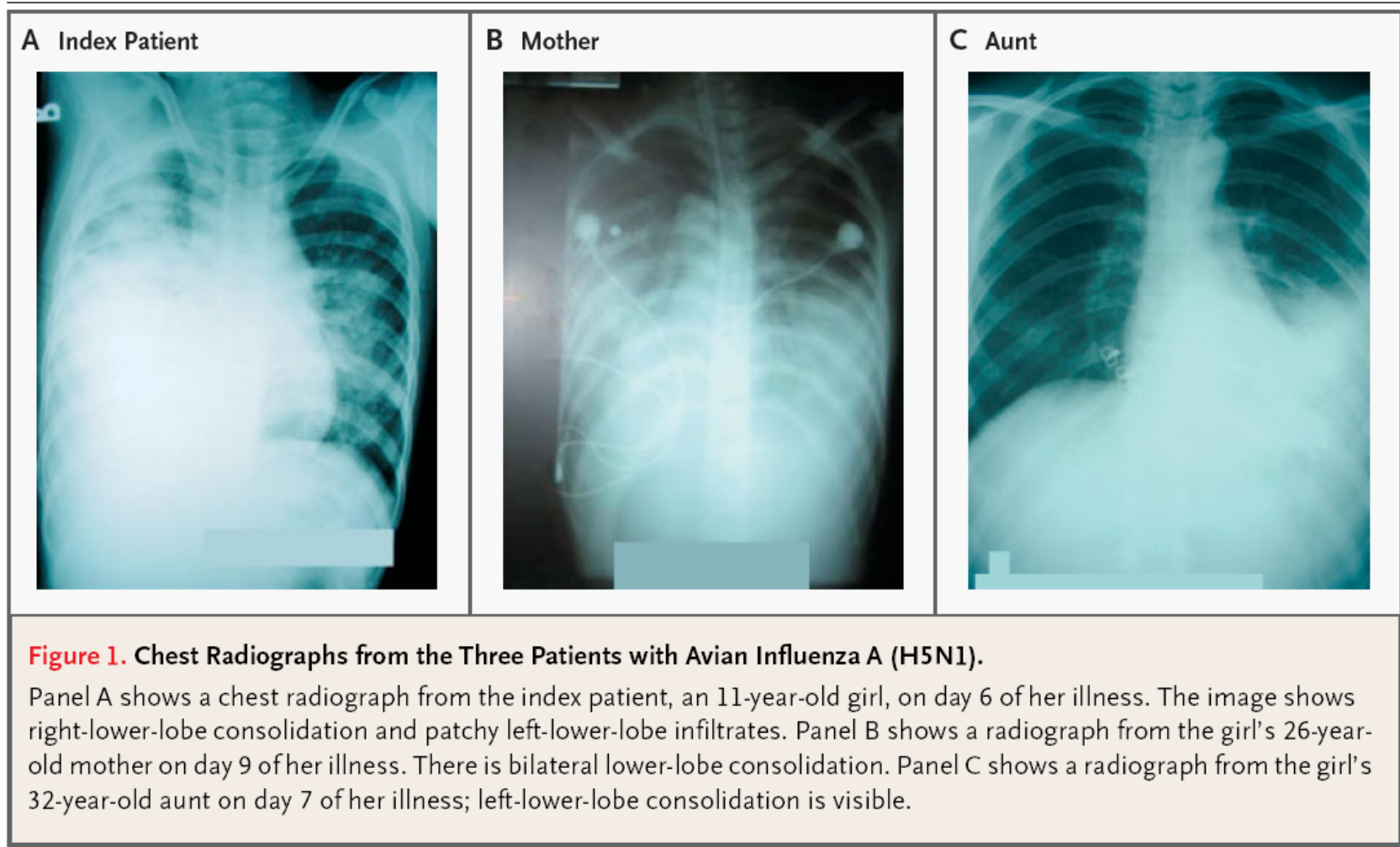
*WHO, World Health Organization. As of September 29, 2005. Source: http://www.who.int/csr/disease/avian_influenza/country/en

**Table 3. Presentation and Outcomes among Patients with Confirmed Avian Influenza A (H5N1).***

Outcome or Measure	Hong Kong, 1997 (N=18)	Thailand, 2004 (N=17)	Vietnam, 2004 (N=10)	Ho Chi Minh City, 2005 (N=10)	Cambodia, 2005 (N=4)
Age — yr					
Median	9.5	14	13.7†	19.4†	22
Range	1–60	2–58	5–24	6–35	8–28
Male sex — no. (%)	8 (44)	9 (53)	6 (60)	3 (30)	1 (25)
Time from last presumed exposure to onset of illness — days					
Median	NS	4	3	NS	NS
Range		2–8	2–4		
No. of family clusters		1	2	1	1
Patients with exposure to ill poultry — no./total no. (%)	11/16 (70) visited poultry markets	14/17 (82)	8/9 (89)	6/6 (100) Status of 4 unknown	3/4 (75)
Time from onset of illness to presentation or hospitalization — days					
Median	3	NS	6	6	8‡
Range	1–7		3–8	4–7	5–8
Clinical presentation — no./total no. (%)					
Fever (temperature >38°C)	17/18 (94)	17/17 (100)	10/10 (100)	10/10 (100)	4/4 (100)
Headache	4/18 (22)	NS	NS	1/10 (10)	4/4 (100)
Myalgia	2/18 (11)	9/17 (53)	0	2/10 (20)	NS
Diarrhea	3/18 (17)	7/17 (41)	7/10 (70)	NS	2/4 (50)
Abdominal pain	3/18 (17)	4/17 (24)	NS	NS	2/4 (50)
Vomiting	6/18 (33)	4/17 (24)	NS	1/10 (10)	0
Cough§	12/18 (67)	16/17 (94)	10/10 (100)	10/10 (100)	4/4 (100)
Sputum	NS	13/17 (76)	5/10 (50)	3/10 (30)	NS
Sore throat	4/12 (33)	12/17 (71)	0	0	1/4 (25)
Rhinorrhea	7/12 (58)	9/17 (53)	0	0	NS
Shortness of breath§	1/18 (6)	13/17 (76)	10/10 (100)	10/10 (100)	NS
Pulmonary infiltrates	11/18 (61)	17/17 (100)	10/10 (100)	10/10 (100)	4/4 (100)
Lymphopenia¶	11/18 (61)	7/12 (58)	NS	8/10 (80)	1/2 (50)
Thrombocytopenia	NS	4/12 (33)	NS	8/10 (80)	1/2 (50)
Increased aminotransferase levels	11/18 (61)	8/12 (67)	5/6 (83)	7/10 (70)	NS



Severe Illness from H5N1





Severe Illness from H5N1

Outcome or Measure	Hong Kong, 1997 (N=18)	Thailand, 2004 (N=17)	Vietnam, 2004 (N=10)	Ho Chi Minh City, 2005 (N=10)	Cambodia, 2005 (N=4)
Hospital course — no. (%)					
Respiratory failure	8 (44)	13 (76)	9 (90)	7 (70)	4 (100)
Cardiac failure	NS	7 (41)	NS	0	NS
Renal dysfunction	4 (22)	5 (29)	1 (10)	2 (20)	NS
Antiviral therapy					
Amantadine	10 (56)	0	0	0	NS
Ribavirin	1 (6)	0	2 (20)	0	
Oseltamivir	0	10 (59)	5 (50)	10 (100)	
Corticosteroids**	5 (28)	8 (47)	7 (70)	5 (50)	NS
Inotropic agents	NS	8 (47)	2 (20)	NS	
Time from onset of illness to death — days					
Median	23	12	9	12.8†	8
Range	8–29	9–30	4–17	4–21	6–10
Deaths — no. (%)	6 (33)	12 (71)	8 (80)	8 (80)	4 (100)



Avoid These



Figure 2. The effect of highly pathogenic H5N1 virus on ducklings in Vietnam (photo T Tumpey).



Table 4. Exposures That May Put a Person at Risk for Infection with Influenza A (H5N1).*

Countries and territories where influenza A (H5) viruses have been identified as a cause of illness in human or animal populations since October 1, 2003

During the 7 to 14 days before the onset of symptoms, one or more of the following:

- Contact (within 1 m) with live or dead domestic fowl or wild birds or domestic ducks
- Exposure to settings in which domestic fowl were confined or had been confined in the previous 6 weeks
- Unprotected contact (within touching or speaking distance) with a person for whom the diagnosis of influenza A (H5N1) is confirmed or being considered
- Unprotected contact (within touching or speaking distance, 1 m) with a person with an unexplained acute respiratory illness that later resulted in severe pneumonia or death
- Occupational exposure†

Countries and territories where influenza A (H5) viruses have not been identified as a cause of illness in human or animal populations since October 1, 2003

During the 7 to 14 days before the onset of symptoms, close contact with an ill traveler from one of the areas with known influenza A (H5) activity, history of travel to a country or territory with reported avian influenza activity due to influenza A (H5N1) in the animal populations, or living in an area in which there are rumors of the death of domestic fowl, and one or more of the following:

- Contact (within 1 m) with live or dead domestic fowl or wild birds in any setting or with domestic ducks
- Exposure to settings in which domestic fowl were confined or had been confined in the previous 6 weeks
- Contact (within touching or speaking distance) with a patient with a confirmed case of influenza A (H5)
- Contact (within touching or speaking distance) with a person with an unexplained acute respiratory illness that later resulted in severe pneumonia or death
- Occupational exposure†

* These summaries do not present formal WHO guidelines, although they contain content from WHO documents.¹

† At-risk occupations include domestic-fowl worker, worker in a domestic-fowl processing plant, domestic-fowl culler (catching, bagging, or transporting birds or disposing of dead birds), worker in a live-animal market, chef working with live or recently killed domestic fowl, dealer or trader in pet birds, health care worker, and a worker in a laboratory processing samples possibly containing influenza A (H5N1) virus.



PI and AI management

- Early suspicion and recognition
- Isolation and testing
- Symptom management
- Neuraminidase inhibitors
 - Oseltamivir (oral) and zanamivir (inhaler)
 - Effective for both influenza A and B (unlike amantadine)
 - Give within 48 hr of symptom onset
 - Prevention of H5N1 but resistance develops rapidly
- Vaccine if available
 - Pandemic influenza vaccine in 2009-2010
 - H5N1 avian influenza vaccine manufactured by Sanofi Pasteur approved by FDA in 2007
 - Testing at NIH for H7N9 avian influenza vaccine



Other Common Respiratory Viruses

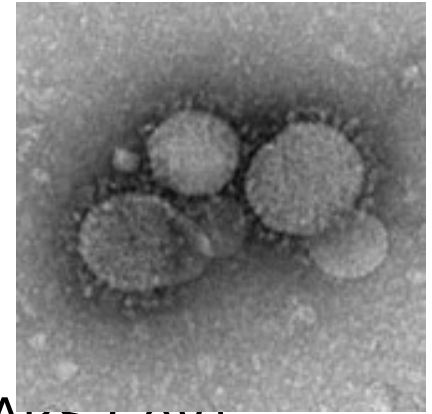
- Respiratory syncytial virus (RSV)
 - Annual epidemics, bronchiolitis in infants
- Human metapneumovirus (HMPV)
 - Similar to RSV
- Parainfluenza virus
 - Four types, type 3 in spring and early summer
- Adenovirus
 - 51 serotypes, types 1-7 responsible for most
 - Oral adenovirus type 4 & 7 vaccine for military
- Rhinoviruses
 - Common cold virus, 100 + serotypes, year-round in tropics
- Coronaviruses
 - Common Cold
 - Severe respiratory infections: SARS CoV (2003), MERS CoV (2013)





Coronavirus

- Meaning 'crown or halo'
- Large, positive sense RNA virus
- Family *Coronaviridae*
- Infects humans, mammals, birds
- Severe acute respiratory syndrome coronavirus (SARS-CoV)
 - Rapid human to human spread worldwide
 - 774 probable deaths, 10% fatality rate
 - Started in Hong Kong Feb. 2003
 - Civet cats and other small mammals to humans ?
 - Delayed peak transmission period
 - Rare within first 5 days of symptom onset
 - Easier recognition, isolation, and interruption
 - No cases since 2004



CDC Image





Middle East Respiratory Syndrome Coronavirus (MERS-CoV)



- Severe, contagious, respiratory illness
- First cluster in Jordan, April 2012
- First Saudi Arabia case, June 2012
- Cluster among family contacts, returning travelers in Europe
- Nosocomial transmission (24% of cases)
- Unidentified reservoir (bats ? camels ?)
- Geographically diverse animal reservoir, initial emergence in July 2011, sporadic introduction into humans and human-to-human transmission

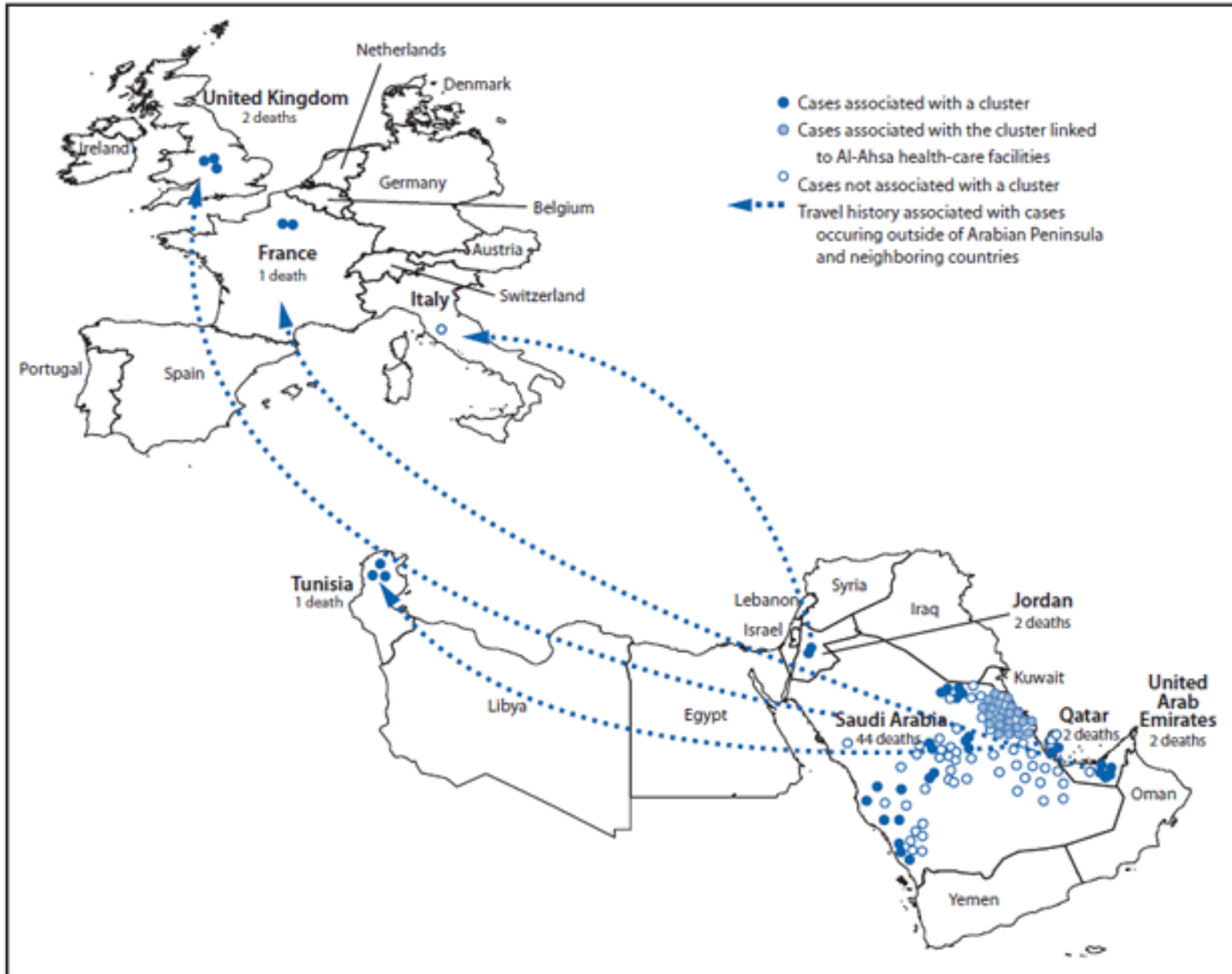


MERS-CoV since April 2012



Countries	Cases (Deaths)
France	2 (1)
Italy	1 (0)
Jordan	2 (2)
Oman	1 (0)
Qatar	7 (3)
Saudi Arabia	125 (53)
Tunisia	3 (1)
United Kingdom (UK)	3 (2)
United Arab Emirates (UAE)	6 (2)
Total	150 (64)

CDC, updated Nov. 6,
2013





Epidemiological, demographic, and clinical characteristics of 47 cases of Middle East respiratory syndrome coronavirus disease from Saudi Arabia: a descriptive study



Lancet Infect Dis 2013;
13: 752–61

Abdullah Assiri*, Jaffar A Al-Tawfiq*, Abdullah A Al-Rabeeh, Fahad A Al-Rabiah, Sami Al-Hajjar, Ali Al-Barrak, Hesham Flenk, Wafa N Al-Nassir, Hanan H Balkhy, Rafat F Al-Hakeem, Hatem Q Makhdoom, Alimuddin I Zumla*, Ziad A Memish*

	Patients (n=47)
Fever	46 (98%)
Fever with chills or rigors	41 (87%)
Cough	39 (83%)
Dry	22 (47%)
Productive (sputum)	17 (36%)
Haemoptysis	8 (17%)
Shortness of breath	34 (72%)
Chest pain	7 (15%)
Sore throat	10 (21%)
Runny nose	2 (4%)
Abdominal pain	8 (17%)
Nausea	10 (21%)
Vomiting	10 (21%)
Diarrhoea	12 (26%)
Myalgia	15 (32%)
Headache	6 (13%)

Table 3: Symptoms of Middle East respiratory syndrome in 47 Saudi cases at presentation

	Patients (n=47)	Deaths (%)*
Any comorbidity	45 (96%)	28 (60%)
Diabetes	32 (68%)	21 (66%)
Chronic kidney disease	23 (49%)	17 (74%)
Chronic heart disease	13 (28%)	10 (77%)
Hypertension	16 (34%)	13 (81%)
Chronic lung disease	12 (26%)	10 (83%)
Obesity	8 (17%)	5 (63%)
Smoking	11 (23%)	7 (64%)
Malignant disease	1 (2%)	1 (100%)
Steroid use	3 (6%)	3 (100%)

*Proportion of patients who died according to comorbidity.

Table 4: Comorbidities in 47 Saudi cases of Middle East respiratory syndrome

MERS Co-V

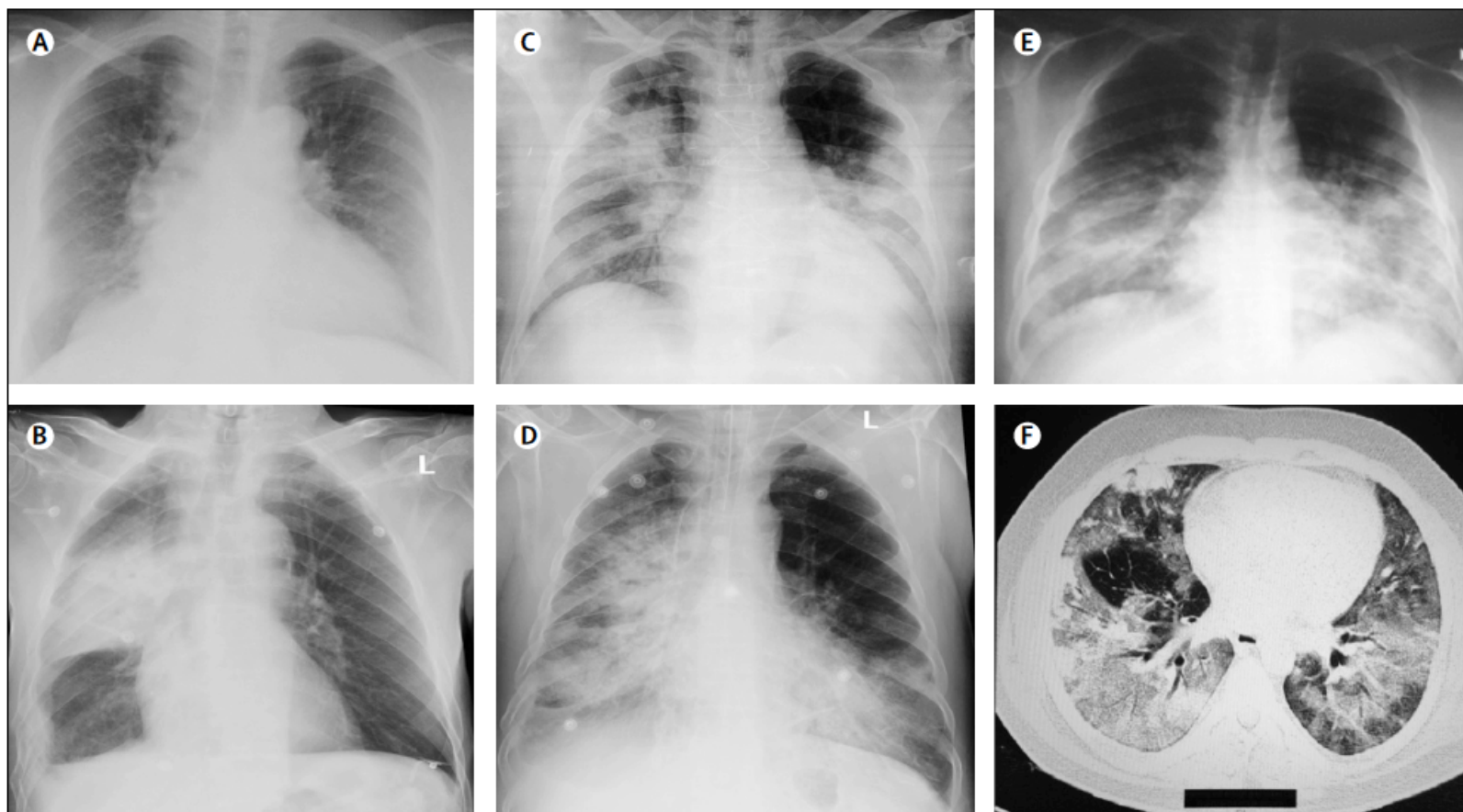


Figure 1: Imaging findings at presentation in Saudi patients with Middle East respiratory syndrome

(A) Chest radiograph of a 61-year-old man, showing bilateral fine reticulonodular air-space opacities, increased vascular markings, and cardiomegaly. (B) Chest radiograph of an 83-year-old man, showing right lung consolidation, right basal pleural thickening, and reticulonodular air-space opacities; rib fractures on the right are old. (C) Chest radiograph of a 56-year-old man, showing extensive bilateral extensive diffuse and focal alveolar space opacities, with opacification of the left lower lobe. (D) Chest radiograph of a 67-year-old man, showing extensive bilateral disease, with diffuse alveolar space densities, opacification, reticulonodular opacities, and bronchial wall thickening. (E) Chest radiograph of a 49-year-old man, showing extensive bilateral mid and lower zone disease, with diffuse reticulonodular alveolar space opacities. A thoracic CT scan in the same patient (F) shows extensive bilateral opacities and ground-glass reticulonodular shadowing and bronchiolar wall thickening.

	MERS-CoV	SARS, global ^{27 34}
Demographic factors		
Date of first case report (place)	April, 2012 (Jordan); June, 2012 (first Saudi case)	November, 2002 (China)
Mean (95% CI) incubation period (days)	5·2 (1·9–14·7); range 2–13	4·6 (3·8–5·8); range 2–14
Serial interval (days)	7·6	8·4
Age distribution	98% adults, 2% children	93% adults, 5–7% children
Mean (range) age (years)	56 (14–94)	39·9 (1–91)
Sex distribution	77% male, 23% female	43% male, 57% female
Sex ratio (male:female)	3·3:1	1:1·3
Clinical features		
Mortality	55%	0–40%
Case-fatality rate (overall)	Undefined	9·6%
In patients with comorbidities	60%	1–2%
Mean time from onset to death (days)	16·5	23·7



Current Guidance – MERS-CoV

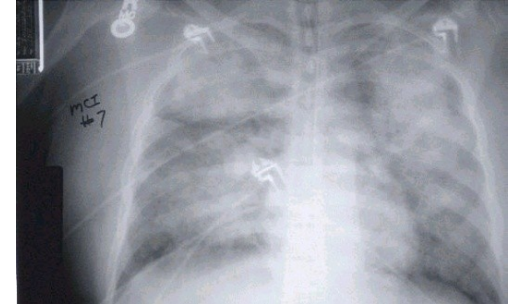
- All cases linked to travel or residence:
 - Saudi Arabia, Qatar, Jordan, United Arab Emirates
- Epidemiology updated by WHO, ECDC, US CDC
- Assess risk, suspect disease
- Lower respiratory tract specimen for rRT-PCR
- Follow up serology testing
- Isolation Precautions
 - Airborne for suspected cases
 - For SARS, CDC: 'airborne precaution preferred'
 - Other standard precautions





Hantavirus Pulmonary Syndrome

- Bunyavirus, enveloped, neg. SS RNA
- New World Hantavirus
 - Approx. 300 cases per year, mortality up to 50%
 - Sporadic cases in the North America: US, Canada
 - Sporadic cases and outbreaks in South America: Argentina, Bolivia, Brazil, Chile, Panama, Paraguay, Uruguay
- Mice and rats are reservoirs
 - Urine, dropping, nesting materials are aerosolized and inhaled by humans
 - Bites and ingestion of contaminated food
 - Barns, outbuildings, and shed are exposure sites
- Incubation 1-4 weeks, initially non-specific myalgia, HA, chills, nausea, vomiting, GI symptoms
- Shortness of breath and cough develops later
 - Rapidly progressive cardiopulmonary phase
 - Bilateral infiltrates, pulmonary edema)
- Conjunctival injection, renal involvement, and hemorrhage reported





Sin Nomore

Peromyscus maniculatus



Muleshoe

Sigmodon hispidus

Isla Vista

Microtus californicus

El Moro Canyon

Reithrodontomys megalotis

Choclo

Oligoryzomys costaricensis

Caño Delgadito

Sigmodon alstoni

Maporal

Oligoryzomys delicatus

Juquitiba

Oligoryzomys nigripes

Rio Mamore

Oligoryzomys microtis

Orán

Oligoryzomys longicaudatus

Bermejo

Oligoryzomys chacoensis

Andes

Oligoryzomys longicaudatus



New World Hantaviruses

New York

Peromyscus leucopus

Prospect Hill

Microtus pennsylvanicus

Bloodland Lake

Microtus ochrogaster

Monongahela

Peromyscus maniculatus

Bayou

Oryzomys palustris

Black Creek Canal

Sigmodon hispidus

Rio Segundo

Reithrodontomys mexicanus

Laguna Negra

Calomys laucha

Araraquara

Bolomys lasiurus

Maciel

Necromys benefactus

Lechiguanas

Oligoryzomys flavescens

Pergamino

Akodon azarae

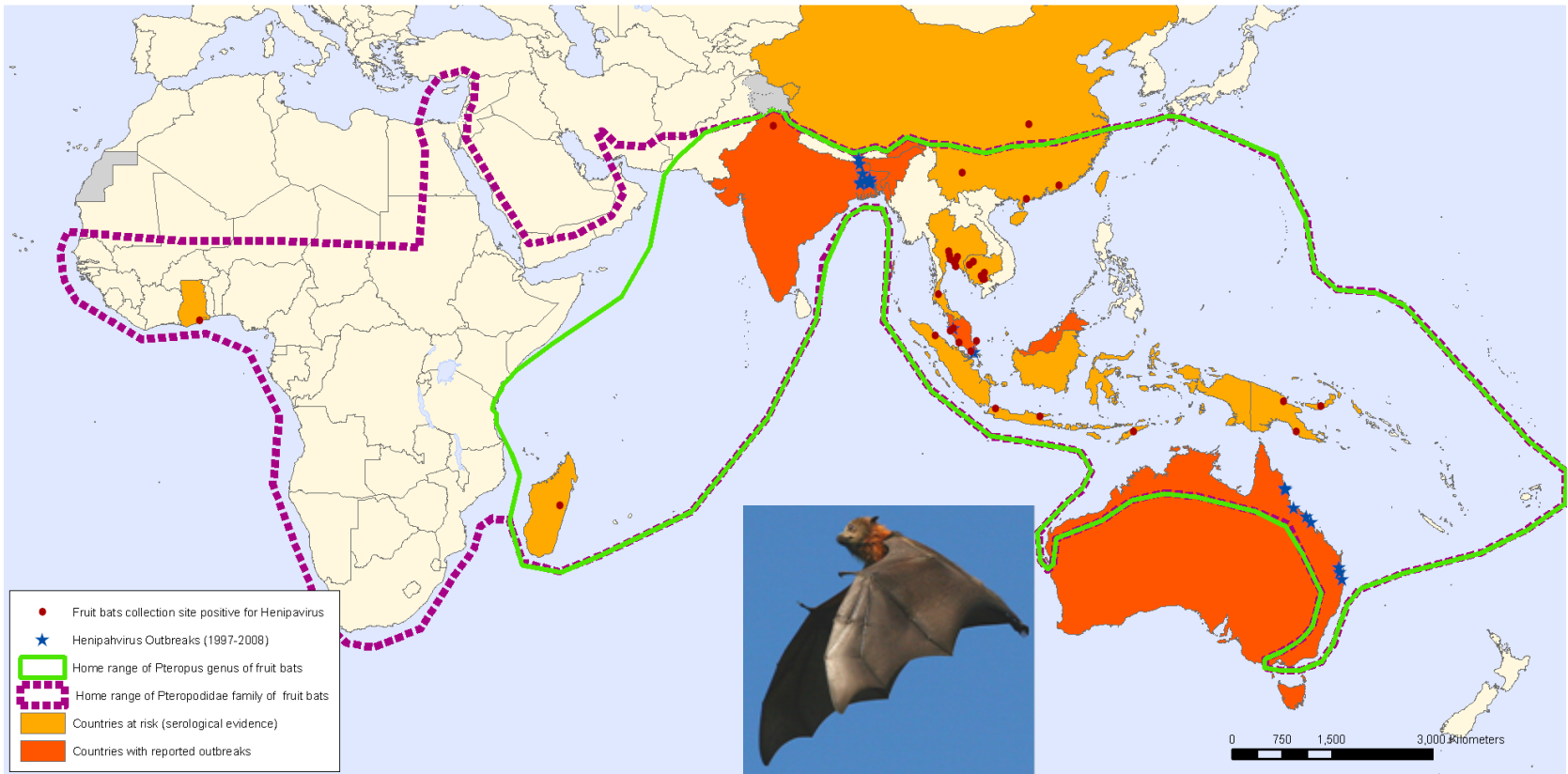


Nipah Virus

- RNA virus, paramyxoviruses, henipavirus
- Recent outbreaks in Malaysia and Bangladesh
- Reservoir are bats in China, SE Asia, India, Madagascar, and Ghana.
- Pigs are hosts
- Humans, cats, dogs infection through direct contact with pig respiratory secretions and urine
- Malaysia outbreak: ? Person to person transmission
- Viral encephalitis with progression to coma, + respiratory symptoms, high mortality

Nipah Virus

Geographic distribution of Henipavirus outbreaks and fruit bats of Pteropodidae Family



The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: Global Alert and Response Department
World Health Organization
Map Production: Public Health Information
and Geographic Information Systems (GIS)
World Health Organization



© WHO 2008. All rights reserved

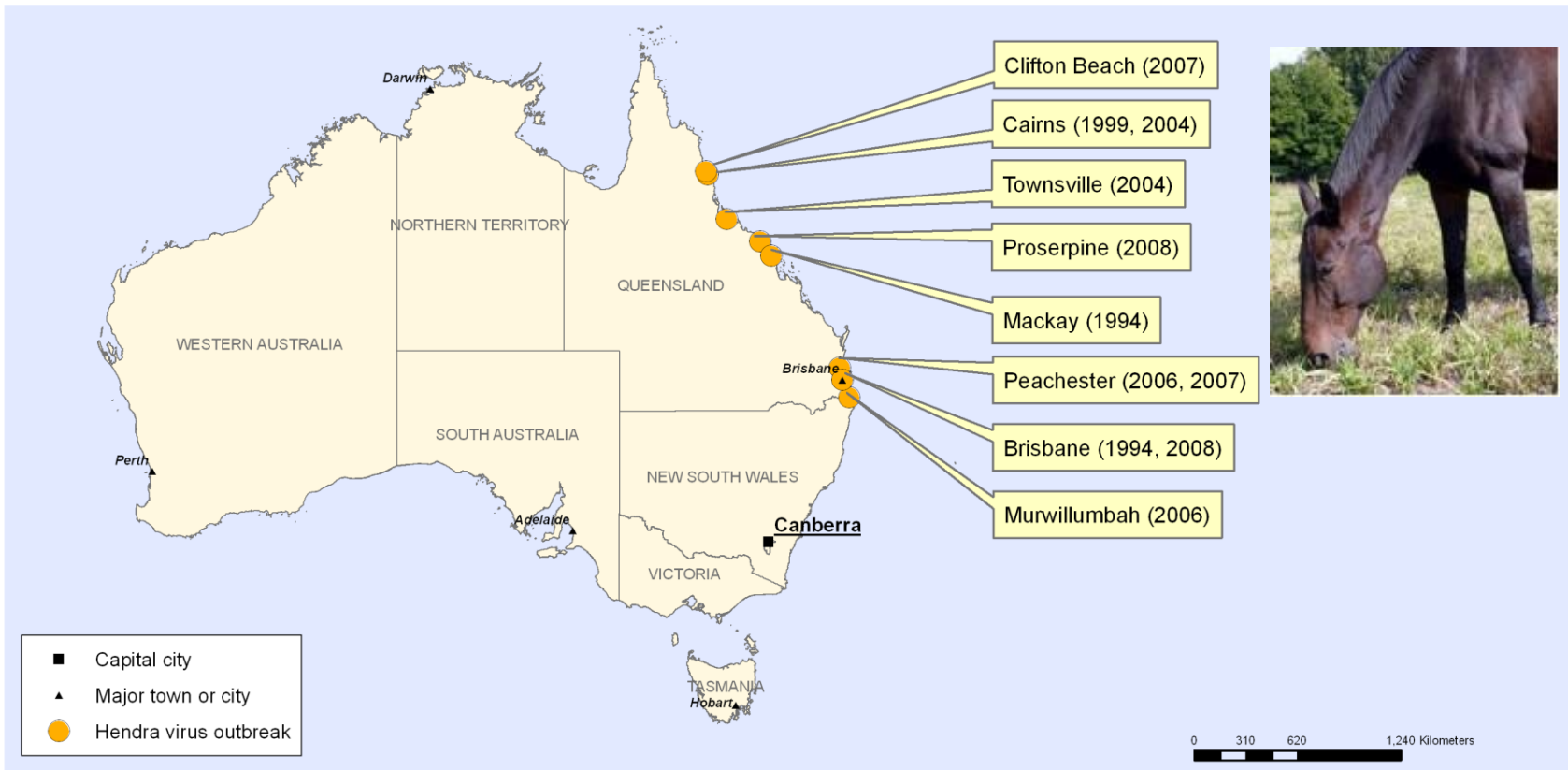


Hendra Virus

- RNA virus, paramyxoviruses, henipavirus
- Bats are the natural reservoir
- Outbreak in horses in Australia
- Four identified human cases in after close contact with horses
 - Two died
- Acute influenza-like illness, meningoencephalitis, seizures, coma

Hendra Virus

Geographic distribution of Hendra virus outbreaks in Australia from 1994 to July 2008



The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: World Health Organization
Map Production: Public Health Information
and Geographic Information Systems (GIS)
World Health Organization



© WHO 2008. All rights reserved



Summary



- Virus are constantly evolving and novel highly virulent respiratory viruses WILL circulate in the future
- An influenza strain that is highly transmissible (H1N1) and highly virulent (H5N1) will likely result in high mortality
- Get vaccinated, protection even when mismatches occur
- Maximize good hand hygiene, distance from others, and personal protective measures
- Consider isolation of patients and assume worst case initially
- Use common sense and avoid contact with animals, local markets, and areas with known outbreaks of respiratory infections



Thank You

Questions ?



Tropical Medicine Course: 'Respiratory Viruses in the Tropics' Lecture Questions:

1). A main difference between the recent H1N1 influenza pandemic and epidemics of avian influenza (H5N1 and H7N9) is:

- a). A vaccine is available for H1N1 whereas avian influenza vaccines are impossible to make
- b). Oseltamivir is only effective for avian influenza but not H1N1
- c). H1N1 is an influenza A virus whereas the avian influenza viruses are influenza B viruses
- d). H1N1 has sustained human to human transmission but this is not true for avian influenza

2). A 24 y.o. SM began experiencing fever, chill, gastrointestinal symptoms, and a cough shortly after returning from a trip in Argentina. After reading about a recent outbreak in Yosemite National Park, you suspect hantavirus as a possible pathogen. Which of the following answers would support your suspicion ?

- a). He visited several rural villages and saw mice
- b). He fed some pigs and explored caves inhabited with bats
- c). He was bitten by several mosquitoes
- d). He rode horses

3). Which of the following is NOT likely to improve overall outcome at your facility when managing a patient with flu-like illness and respiratory symptoms for 4 days who recently visited Saudi Arabia ?

- a). Closely monitor those who came in contact or traveled with the sick individual
- b). Start oseltamivir immediately on the patient
- c). Airborne precautions for the patient and N-95 mask for visitors if available or at minimum droplet precautions
- d). Obtain lower respiratory tract specimens for testing for MERS-CoV

Answers: D, A,
B